

	Query Match	11.5%	Score 81.5	DB 22	Length 945
Best Local Similarity	28.3%				
Pred. No. 10					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					
Matches 30					
Conservative 14					
Mismatches 37					
Indels 25					
Gaps 5					

RESULT 5	
AAE19157	
ID	AAE19157 standard; Protein; 945 AA.
XX	
AC	AAE19157;
XX	
DT	21-MAY-2002 (first entry)
XX	
DE	Human kinase polypeptide (PKIN-15).

Human; kinase polypeptide; PKIN-15; gene therapy; Addison's disease; leukaemia; immune disorder; lymphoma; melanoma; developmental disorder; acquired immunodeficiency syndrome; AIDS; allergy; anaemia; hypertension; asthma; Crohn's disease; rheumatoid arthritis; bursitis; atherosclerosis; cirrhosis; hepatitis; psoriasis; Cushing's syndrome; cytostatic; cancer; cholestasis; cardiac; cardiovascular disorder; Niemann-Pick's disease; lipid disorder; fatty liver; Gaucher's disease; myocardial infarction; drug screening; transgenic animal; anti-inflammatory; hepatotropic; hypotensive; anti-HIV; enzyme.

Key	Location/Qualifiers
FFH	661..920
FFFT	/note= "Eukaryotic protein kinase domain"
FF	
FTT	
XX	
PN	WO200208399-A2.
XX	
XX	
CD	31-JAN-2002.
XX	
XX	20-JUL-2001; 2001WO-US23092.
PF	

21-JUL-2000; 2000US-220038P.
28-JUL-2000; 2000US-222112P.
04-AUG-2000; 2000US-222831P.
11-AUG-2000; 2000US-224729P.
XX (INCY-) INCYTE GENOMICS INC.
PA (THOR/) THORNTON M.
PA

Thornton M, Yue H, Khan FA, Gururajan R, Hafalia AJA, Wallia NK;
Patterson C, Ramkumar J, Gandhi AR, Policky JL, Baughn MR;
Tribouley CM, Bandman O, Nguyen DB, Lu Y, Burford N, Lal P;
Ding L, Yao MG, Elliott VS, Recipson SA, Kearney L, Lu DAM;
Greenwald SR, Tang YT, Xu Y, Walsh RT, Gietzen KJ, Yang J;
Hillman JL;
WPI: 2002-206083/26.
N-PSDB: AAD30562.
New human kinase polypeptide, useful in diagnosis, prevention and
treatment of cancer, immune disorder, growth and developmental
disorder, cardiovascular disorder and lipid disorder -
Claim 1; Page 155-157; 196pp; English.

The present invention relates to an isolated human kinase polypeptide (PKIN) or a biologically active/immunogenic fragment of PKIN. PKIN is useful for diagnosing, treating and preventing cancer (e.g., leukemia, lymphoma, melanoma), an immune disorder (e.g., acquired immunodeficiency).

CC syndrome (AIDS), Addison's disease, allergy, anaemia, asthma, Crohn's
 CC disease, rheumatoid arthritis), a growth and developmental disorder (e.g.
 CC buritis, cirrhosis, hepatitis, psoriasis, Cushing's syndrome), a
 CC cardiovascular disorder (e.g., atherosclerosis, hypertension, myocardial
 CC infarction), and a lipid disorder (e.g., fatty liver, cholestasis,
 CC Gaucher's disease, Niemann-Pick's disease). PKIN is useful in a number of
 CC drug screening techniques and to analyse the proteome of a tissue or cell
 CC type. PKIN is useful for creating knockin humanised animals or transgenic
 CC animals to model human diseases, in somatic or germline gene therapy, to
 CC generate a transcript image of a tissue or cell type, for detecting
 CC differences in the chromosomal location due to translocation, inversion,
 CC etc., among normal, carrier or affected individuals, and as hybridisation
 CC probes for mapping naturally occurring genomic sequences. PKIN is useful
 CC in southern or northern analysis, dot blot or other membrane-based
 CC technologies, in PCR technologies, in dipstick, pin, microarray enzyme
 CC linked immunosorbent (ELISA)-like assays and in microarrays utilising
 CC fluids or tissues from patients to detect altered PKIN expression. The
 CC present sequence is human PKIN-15.
 XX
 XX Sequence 945 AA;
 SQ
 Query Match 11.5%; Score 81.5; DB 23; Length 945;
 Best Local Similarity 28.3%; Pred. No. 10;
 Matches 30; Conservative 14; Mismatches 37; Indels 25; Gaps 5;
 QY 43 ALAGMC-----GHRVLPGTGASA-----IAATVTPKGA-----SMKLLKPPRP 79
 Db 226 AYPGLCPPLPPLSGHSLPPSPQRHAYVTPRTNIVTTPPTPMRKNKLLKPPGT 285
 QY 80 QSTKGPSELRSKIRENMNTIQSARVNHRLPEGH-PLLEKRAE 124
 Db 286 PPPSSRKLIHLIPGFTALHRSHE-FOLGHRVDEAHTPKAKKSK 330
 RESULT 6
 ABB61917
 ID ABB61917 standard; Protein; 1259 AA.
 AC ABB61917;
 XX
 XX 15-AUG-2002 (first entry)
 DT
 DE Prostate cancer-associated protein #118.
 XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
 KW
 OS Mammalia.
 XX
 XX WO200230268-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US32045.
 XX
 PR 13-OCT-2000; 2000US-0687576.
 PR 08-DEC-2000; 2000US-0733288.
 PR 08-DEC-2000; 2000US-0733742.
 PR 24-JAN-2001; 2001US-263957P.
 PR 16-MAR-2001; 2001US-276791P.
 PR 16-MAR-2001; 2001US-276888P.
 PR 06-APR-2001; 2001US-281322P.
 PR 24-APR-2001; 2001US-286214P.
 PR 30-APR-2001; 2001US-0847046.
 PR 04-MAY-2001; 2001US-288589P.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
 PI WPI; 2002-471335/50.
 XX N-PSDB; ABK92234.
 DR
 XX
 XX Detecting a prostate cancer-associated transcript in a cell in a

PT patient, useful for diagnosing prostate cancer (PC) or screening
 PT modulators of PC, by determining if prostate cancer-associated genes
 PT are expressed in a prostate tissue
 XX
 XX Claim 27; Page 401; 436pp; English.
 XX
 CC The present invention relates to methods of detecting a prostate
 CC cancer-associated transcript in a cell from a patient. The method
 CC comprises contacting a biological sample from the patient with
 CC prostate cancer-associated polynucleotides (designated PC genes) that
 CC selectively hybridise to a sequence that is at least 80% identical
 CC to them. The prostate cancer-associated polynucleotide sequences
 CC are differentially expressed in prostate tumour tissue or in
 CC prostate cancer and are derived from the tissues of various
 CC organisms such as humans or other mammals (e.g. mice, sheep and dogs).
 CC The methods of the invention are useful for diagnosing and treating
 CC prostate cancer in mammals. The prostate cancer-associated genes are
 CC useful for diagnosing or treating prostate cancer, as well as for
 CC identifying modulators of prostate cancer or agents that inhibit
 CC prostate cancer. The nucleic acid sequences are particularly useful
 CC in gene therapy, as a vaccine or in antisense applications.
 CC ABB61800-ABG61944 represent prostate cancer-associated proteins.
 XX
 XX Sequence 1259 AA;
 SQ
 Query Match 11.5%; Score 81.5; DB 23; Length 1259;
 Best Local Similarity 26.8%; Pred. No. 14;
 Matches 37; Conservative 17; Mismatches 43; Indels 41; Gaps 6;
 QY 20 ETDVMEALLRVKSSERLAMLRA-----LAGMCGHRVLPGTG-----ASAIA 62
 Db 655 EQLDAINKEIRLIQEKESTELRAEINERVASVLEGLNARVHPTCSITASVTASSLA 714
 QY 63 ATVTPKGASM-KLKPPRPQ-----STKSPLELRSRKI-----REMNTISOESA 106
 Db 715 SSSPPSGHSTPKLTSPSPAREMDRMGMVMTLPDLRKHRRIAYVEEDGREDKATIKETS 774
 QY 107 -----RVNHLPEGH 116
 Db 775 PPTPRALRMTHTLPSY 792
 RESULT 7
 ABB63351
 ID ABB63351 standard; Protein; 1157 AA.
 XX ABB63351;
 XX
 XX 26-MAR-2002 (first entry)
 DT
 XX Drosophila melanogaster polypeptide SEQ ID NO 16845.
 XX DE
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX Drosophila melanogaster.
 XX
 XX WO200171042-A2.
 XX
 XX 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 XX 11-JUL-2000; 2000US-0614150.
 PR
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 DR N-PSDB; ABL07454.
 XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PS Disclosure; SEQ ID NO 16845; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABU16176-ABU16051), expressed DNA
CC sequences (ABU16176-ABU16175) and the encoded proteins
CC (ABU16176-ABU16051).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1157 AA;

Query Match 11.4%; Score 80.5; DB 22; Length 1157;
Best Local Similarity 28.4%; Pred. No. 17;
Matches 25; Conservative 13; Mismatches 37; Indels 13; Gaps 3;
QY 55 GTGASAIATVTPKGAS--MKLKPRP-----QSTKSPPELRLSR--KIREMNKTI 101
DB ||||| : : : : : ||||| : : : : : ||||| : : : : :
462 GTGTGSDYRSRPTSTSRMTSESSPVGASGSHYHRRSPRMRQTRGDSRRSPSSA 521
QY 102 SQESARVNHRLPECHPLLEKRAEYERHL 129
DB ||||| : : : : : ||||| : : : : : ||||| : : : : :
522 SSESASRSRSPTRDLXHKREYIKKI 549

RESULT 8
ID AAY01973 standard; Protein; 192 AA.
XX
AC AAY01973;
XX
DT 02-JUL-1999 (first entry)
XX
DE HIV-1 viral infectivity factor protein N23.
XX
KW Consensus sequence; attenuated; non-functional; accessory protein; vif;
KW viral infectivity factor; HIV-1; vaccine.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO9913896-A1.
XX
PD 25-MAR-1999.
XX
PF 18-SEP-1998; 98WO-US19478.
XX
PR 26-SEP-1997; 97US-0060172.
PR 18-SEP-1997; 97US-0059283.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Ayyavoo V, Nagashunmugam T, Weiner DB;
XX
DR WPI; 1999-263380/22.
DR N-PSDB; AAX35221.
XX
PT New attenuated vif (viral infectivity factor) genes, used in genetic
XX vaccines against HIV-1
XX
PS Claim 2; Page 63; 92pp; English.
XX
CC The specification describes novel vif proteins (AAY01969-88) and
CC the genes encoding them (AAX35217-36). The vif gene is an accessory gene
CC for HIV-1 that has low functional mutagenicity and is conserved. In
CC addition, attenuated, non functional vif clones are able to induce

CC immune responses capable of destroying native pathogen. Vif nucleic
CC acids may be used to immunize mammals. The attenuated, non-functional
CC vif genes may be used in concert with other HIV-1 genes to produce
CC vaccine that has a broad immune response against all viral
CC components, and which mimics many aspects of the immune responses
CC induced by a live attenuated virus. Prophylactic vaccines which include
CC vif could limit both viral escape and contribute to lowering the viral
CC set point during early infection stages.
XX
SQ Sequence 192 AA;

Query Match 11.2%; Score 79; DB 20; Length 192;
Best Local Similarity 29.9%; Pred. No. 2.4;
Matches 32; Conservative 9; Mismatches 28; Indels 38; Gaps 6;

QY 22 FVDMREALLRVKSSERLAWLRALAGMCHRVLP---GTGAS-----AIAATVTPKG 69
DB || : : : : : ||||| : : : : : ||||| : : : : :
112 FCLSESAR-----KAILGHRVSPCEYRAGHSKVGSLQYLAIALLTPK- 157

QY 70 ASMKLKPPRPOSTKSPPELRLSRKIREMNKTIQSARVNHRLPEGH 116
DB ||||| : : : : : ||||| : : : : : ||||| : : : : :
158 ---KIKPLPSVRKLTEDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 9
ID ABUS3201 standard; Protein; 1780 AA.
XX
AC ABUS3201;
XX
DT 14-APR-2003 (first entry)
XX
DE Human cell cycle-associated protein from DKFZphtes3_35b4.
XX
KW Human; gene therapy; vaccine; disease treatment; detection.
XX
OS Homo sapiens.
XX
PN WO200112659-A2.
XX
PD 22-FEB-2001.
XX
PF 18-AUG-2000; 2000WO-IE01496.
XX
PR 18-AUG-1999; 99US-0149499.
PR 28-SEP-1999; 99US-0158503.
XX
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
XX
PI Wiemann S;
XX
DR WPI; 2001-327840/34.
DR N-PSDB; ABX71393.
XX
PT Nucleic acids having the sequences of clones isolated from libraries of
PT different human tissues, useful in recombinant DNA methodologies -
XX
PS Claim 21; Page 821; 1095pp; English.
XX

CC This invention describes novel polynucleotides and polypeptides isolated
CC from human cDNA libraries which can be used for gene therapy or in
CC vaccines. The polynucleotides of the invention and antibodies encoded by
CC them may be used in the prevention, diagnosis and treatment of diseases
CC associated with inappropriate polypeptide expression. The products of the
CC invention may also be used to identify modulators of expression and
CC activity and to down regulate expression and activity. The antibodies of
CC the invention may also be used as diagnostic agents for detecting the
CC presence of polypeptides in samples. This sequence represents a
CC polypeptide described in the disclosure of the invention.
XX
SQ Sequence 1780 AA;

Query Match 11.2%; Score 79; DB 22; Length 1780;

Best Local Similarity 21.3%; Pred. No. 42; Mismatches 27; Conservative 27; Indels 14; Gaps 2;
Matches 32; Conservative 27; Mismatches 27; Indels 14; Gaps 2;
QY 2 ESTSTTTNFAENRPTGTFDVMREALLRVKSSERLALAGMCHGHRVLPOTGASAI 61
Db 604 EYTQFTQYWAQREADPKETLLQERE-ILEENAERRLAIFKDLVGKCDTREAAKDICAT 662
QY 62 AATVTPKGASMKLPKPPRPOSTKSPELRELSRKIREMNKTSIQESARV----- 108
Db 663 KVETEATACLELKFNOIKAEIAKTKGELIKTKRENESSDLSIQELETNSKKIITQ 722
QY 109 NHRLEPGHPLLEKRAEYFRHLRSLKSGQVN 138
Db 723 NQRIKELINIIDQKEDTINEFQNLKSHMEN 752
RESULT 10
AAM38681
ID AAM38681 standard; Protein; 1780 AA.
AC AAM38681;
XX
DT 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 1826.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSEQ-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI57837.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Example 3; SEQ ID NO 1826; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic, and
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 1780 AA;
Query Match 11.2%; Score 79; DB 22; Length 1780;
Best Local Similarity 21.3%; Pred. No. 42;
Matches 32; Conservative 27; Mismatches 27; Indels 14; Gaps 2;
QY 2 ESTSTTTNFAENRPTGTFDVMREALLRVKSSERLALAGMCHGHRVLPOTGASAI 61
Db 604 EYTQFTQYWAQREADPKETLLQERE-ILEENAERRLAIFKDLVGKCDTREAAKDICAT 662
QY 62 AATVTPKGASMKLPKPPRPOSTKSPELRELSRKIREMNKTSIQESARV----- 108
Db 663 KVETEATACLELKFNOIKAEIAKTKGELIKTKRENESSDLSIQELETNSKKIITQ 722
QY 109 NHRLEPGHPLLEKRAEYFRHLRSLKSGQVN 138
Db 723 NQRIKELINIIDQKEDTINEFQNLKSHMEN 752
RESULT 11
AAM40467
ID AAM40467 standard; Protein; 1788 AA.
AC AAM40467;
XX
DT 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 5398.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSEQ-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI59623.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX

PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX Claim 20; SEQ ID No 59462; 103pp; English.
 XX
 XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridization probes,
 CC polymerase chain reaction (PCR) primers, oligomers and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 XX Sequence 828 AA;

Query Match 11.1%; Score 78.5; DB 22; Length 828;
 Best Local Similarity 24.0%; Pred. No. 18;
 Matches 24; Conservative 16; Mismatches 41; Indels 19; Gaps 2;
 QY 4 TTTTNFVAENPTGTEFDVNRALLRVKSSERLAMLALAGMCGHRVLPOTGASATAA 63
 DB 228 TTTTLRLVIRLVGAYGSDLEKVRKVLKAAATGHRVM-----HSPMPEVPTAFGA 278
 QY 64 TVTPKASMKLPPRPQSTKSPELRELSKIREMKNKTISQ 103
 DB 279 SLIDHELRLYVR-----ELDRSRVTDELNRITDQ 308

RESULT 14
 AAP60348
 ID AAP60348 standard; protein; 203 AA.
 XX AAP60348;
 AC AAP60348;
 XX 25-MAR-2003 (updated)
 DT 01-JAN-1980 (first entry)
 XX
 XX HTLV-III virus (HIV virus) sor protein.
 DE
 XX HTLV-III; HIV virus; AIDS; active immunization; sor protein;
 KW passive immunization; vaccine; ss.
 XX
 XX HIV virus (HTLV-III).
 OS
 XX EP185444-A.
 PN
 XX 25-JUN-1986.
 PD
 XX 10-OCT-1985; 8SEP-0307260.
 PF
 XX 23-JAN-1985; 85US-0693866.
 PR 10-OCT-1984; 84US-0659339.
 XX
 XX (CENZ) CENTOCOR INC.
 PA (USSH) NAT INST OD HEALTH.
 XX
 XX Chang NT;
 PI
 XX WPI; 1986-163443/26.
 DR

DR N-PSDB; AAN60240.
 XX
 XX New immunoreactive HTLV-III polypeptide expressed by transformed
 PT cells - and derived antibodies, useful for diagnosis of AIDS and
 PT in active or passive immunisation
 XX
 XX Disclosure; Fig. 3; 60pp; English.
 XX
 XX HIV virus cDNA is cleaved with restriction endonucleases to produce
 CC the gag protein. The resulting protein and antibodies against it
 CC are useful for immunosay of HIV virus, e.g. by sandwich type RIA.
 CC The protein may also be used in vaccines for active immunization.
 CC See also AAP60346-7 and AAP60349.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX Sequence 203 AA;

Query Match 11.0%; Score 78; DB 7; Length 203;
 Best Local Similarity 27.9%; Pred. No. 3.3;
 Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;
 QY 22 FDMREALLRVKSSERLAMLALAG-----MCGHRVLPOTGASATVTPKASGM 72
 DB 123 FDFSDSAIR-----KALLGHIVSPRCYQAGHNKVGSLQYLALALITPK---- 168
 QY 73 XLKPPRPQSTKSPELRELSKIREMKNKTISQESARVNHRLPEGH 116
 DB 169 KIKPPLPSVTKLTEER-----WNKPQTKGHRGSHTW-NGH 203

RESULT 15
 ABB68134
 ID ABB68134 standard; Protein; 409 AA.
 XX ABB68134;
 AC ABB68134;
 XX 26-MAR-2002 (first entry)
 DT
 XX Drosophila melanogaster polypeptide SEQ ID NO 31194.
 DE
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 KW
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 FN
 XX 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 PR
 XX (PEKE) PE CORP NY.
 PA
 XX Venter JC, Adams M, Li PWD, Myers EW;
 PI
 XX WPI; 2001-656860/75.
 DR N-PSDB; ABL12237.
 XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 XX Disclosure; SEQ ID NO 31194; 21pp + Sequence Listing; English.
 XX
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.
XX
SQ Sequence 409 AA;

Query Match 10.9%; Score 77.5; DB 22; Length 409;
Best Local Similarity 33.3%; Pred. No. 9.3;
Matches 26; Conservative 13; Mismatches 28; Indels 11; Gaps 3;

QY 59 SAIAATVTPKASMKLKPDPQSTKSPPELRLSKIREMNTKISQESARVNHRLPEGH 118
DB 14 AAVLMTATROGHTIRGPP-----GVARSLEGRIREENVPEVVARINIGFPQ---L 63

QY 119 LEKR-AYEVRHLRLSKSQ 135
DB 64 KESRSQAQLKXRLHLXSQ 81

RESULT 16
ABB83793
ID ABB83793 standard; Protein; 451 AA.
XX
AC ABB83793;
XX
DT 29-AUG-2002 (first entry)
XX
DE Fungal decaprenyl diphosphate synthase SEQ ID NO 4.
XX
KW Fungi; Aspergillus; Leucosporidium; coenzyme Q10; enzyme;
KW decaprenyl diphosphate synthase; enzyme.
XX
DS Aspergillus clavatus.
XX
PN WO200252017-A1.
XX
PD 04-JUL-2002.
XX
PF 27-DEC-2001; 2001WO-JP11523.
XX
PR 27-DEC-2000; 2000JP-0398658.
XX
PA (KANF) KANEKA CORP.
XX
PI Matsuda H, Kawamukai M, Yajima X, Ikenaka Y;
XX
JR WPI; 2002-500767/53.
XX
DR N-PSDB; AEN81605.
XX
XT Microbial production of coenzyme Q10 by transformants transferred with
XT fungal decaprenyl diphosphate synthase gene, on industrial scale for
XT application in drugs -
XX
XS Claim 4; Page 37-40; 52pp; Japanese.
XX
XC The invention relates to a DNA sequence (I, AEN81604-ABN81605),
XC containing a sequence based on that of (I) but with some bases deleted,
XC added, inserted and/or substituted and encoding a protein
XC (ABB83792-ABB83793) with decaprenyl diphosphate synthase activity or
XC hybridisable with (I) under stringent conditions and encoding a protein
XC with decaprenyl diphosphate synthase activity. The DNA is useful for the
XC production of coenzyme Q10 for application in drugs. The coenzyme is
XC simply produced on industrial scale, efficiently, with significantly
XC productivity.
XX
Q Sequence 451 AA;

Query Match 10.9%; Score 77.5; DB 23; Length 451;
Best Local Similarity 29.6%; Pred. No. 10;
Matches 24; Conservative 12; Mismatches 28; Indels 17; Gaps 3;

QY 57 GASAIATVTPKASMKLKPDPQSTKSPPELRLSKIREMNTKISQESARVNHRLPEGH 116
DB 56 GAASAAQTIFKGL-----PKAPPGISVDPRLRVGKELFELTKNIHQ-----LLGSGH 103

QY 117 PLEKRAEYF-----RHLRSL 132
DB 104 PTLQKVAKYTRSEGHMRPL 124

RESULT 17
AAW94135
ID AAW94135 standard; peptide; 96 AA.
XX
AC AAW94135;
XX
DT 13-APR-1999 (first entry)
XX
DE VIF-derived HIV protease inhibitor C'vif (residues 97-192).
XX
KW Protease inhibitor; lentiviral; retroviral; replication; Vif protein;
KW simian immunodeficiency virus; feline immunodeficiency virus; HIV-1;
KW bovine immunodeficiency virus; infection; HIV-2.
XX
OS Synthetic.
OS Human immunodeficiency virus type 1.
XX
PN WO9852970-A1.
XX
PD 26-NOV-1998.
XX
PF 20-MAY-1998; 98MO-US10307.
XX
PR 20-MAY-1997; 97US-0047200.
XX
PA (SLUK-) ST LUKE'S ROOSEVELT HOSPITAL.
XX
PA (YISS) YISSUM RES & DEV CO.
XX
PI Kotler M, Volsky DJ;
XX
JR WPI; 1999-059738/05.
XX
PT New protease inhibitors comprising a sequence of lentiviral vif -
PT which inhibit lentiviral replication, used for treating or
PT preventing infection, particularly by HIV
XX
PS Example 1; Page 31; 108pp; English.
XX
CC The invention provides protease inhibitors which inhibit lentiviral or
CC retroviral replication where the inhibitor comprises an amino acid
CC sequence which corresponds to an amino acid sequence in a lentiviral
CC vif protein. The protease inhibitors can be used for the prevention or
CC treatment of lentiviral or retroviral infection, e.g. those resulting
CC from HIV-1, HIV-2, simian immunodeficiency virus, feline immunodeficiency
CC virus, bovine immunodeficiency virus. DNA encoding the peptides can also
CC be used in such methods. The present sequence represents an example of a
CC peptide inhibitor of the invention derived from the HIV-1 Vif protein.
XX
SQ Sequence 96 AA;

Query Match 10.9%; Score 77; DB 20; Length 96;
Best Local Similarity 27.9%; Pred. No. 1.6;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

QY 22 FDMVEALLRVKSSERLAMLRLAG-----MCGRVLPFGTASAIATVTPKASGM 72
DB 16 FDFGSDSAIR-----KALLGHIVSPCEVQAGHNKVGSLQYLALALITPK---- 61

QY 73 KLKPPRQSTKSPPELRLSKIREMNTKISQESARVNHRLPEGH 116
DB 62 KIKPLPSVTKLTEDR-----WNKPQTKGHRSHSTM-NGH 96

RESULT 18

```

AAV01976
ID   AAY01976 standard; Protein; 192 AA.
XX
XX   AAY01976;
XX
XX   DT      02-JUL-1999 (first entry)
XX
XX   DE      HIV-1 viral infectivity factor protein N27.
XX
XX   KW      Consensus sequence; attenuated; non-functional; accessory protein; vif;
XX           viral infectivity factor; HIV-1; vaccine.
XX
XX   OS      Human immunodeficiency virus type 1.
XX
XX   PN      WO9913896-A1.
XX
XX   PD      25-MAR-1999.
XX
XX   PF      18-SEP-1998; 98WO-US19478.
XX
XX   PR      26-SEP-1997; 9TUS-0060172.
XX           18-SEP-1997; 9TUS-0059283.
XX
XX   PA      (UYPE-) UNIV PENNSYLVANIA.
XX
XX   PY      Aygavoo V, Nagashunmugam T, Weiner DB;
XX
XX   WP      WI; 1999-263380/22.
XX           N-PSDB; AAX35224.
XX
XX   PT      New attenuated vif (viral infectivity factor) genes, used in genetic
XX           vaccines against HIV-1
XX
XX   PS      Claim 2; Fig 7B-C; 92pp; English.
XX
XX   CC      The specification describes novel vif proteins (AAY01969-88) and
CC           the genes encoding them (AAX35217-36). The vif gene is an accessory gene
CC           for HIV-1 that has low functional mutagenicity and is conserved. In
CC           addition, attenuated, non functional vif clones are able to induce
CC           immune responses capable of destroying native pathogen. vif nucleic
CC           acids may be used to immunize mammals. The attenuated, non-functional
CC           vif genes may be used in concert with other HIV-1 genes to produce
CC           vaccine that has a broad immune response against all viral
CC           components, and which mimics many aspects of the immune responses
CC           induced by a live attenuated virus. Prophylactic vaccines which include
CC           vif could limit both viral escape and contribute to lowering the viral
CC           set point during early infection stages.
XX
XX   SQ      Sequence 192 AA;

Query Match          10.9%; Score 77; DB 20; Length 192;
Best Local Similarity 29.9%; Pred. No. 4;
Matches 32; Conservative 8; Mismatches 29; Indels 38; Gaps 6;

QY    22 FDVMREALLRVKSSERLAMLRLAGMCGHRVLPL-----GTGAS-----ATAATVPKG 69
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db    112 FDCFSESAIR-----KAILGHRVSPRCEYRAGHSKYCSLOYLAIALIITPK- 157

QY    70 ASMKLKPPROSQTSKPLRLSRKIREMNKTISQESARVNHLREGH 116
      ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db    158 ---KIKPPLPSVRKLTEDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 19
AAY01977
ID   AAY01977 standard; Protein; 192 AA.
XX
XX   AC      AAY01977;
XX
XX   DT      02-JUL-1999 (first entry)
XX
XX   DE      HIV-1 viral infectivity factor protein N29.
XX
XX           DE
XX

```

KW	Consensus sequence; attenuated; non-functional; accessory protein; vif;
XX	viral infectivity factor; HIV-1; vaccine.
XX	Human immunodeficiency virus type 1.
XX	WO9913896-A1.
XX	PN
XX	25-MAR-1999.
PD	
XX	18-SEP-1998; 98WO-US19478.
XX	26-SEP-1997; 97US-0060172.
XX	18-SEP-1997; 97US-0059283.
XX	(UYPE-) UNIV PENNSYLVANIA.
PA	
XX	Ayyavoo V, Nagashumugam T, Weiner DB;
PI	
XX	WPI; 1999-263380/22.
DR	N-PSDB; AAX35225.
DR	
XX	New attenuated vif (viral infectivity factor) genes, used in genetic
PT	vaccines against HIV-1
XX	
PS	Claim 2; Fig 7C; 92pp; English.
XX	
CC	The specification describes novel vif proteins (AAY01969-88) and
CC	the genes encoding them (AAX35217-36). The vif gene is an accessory gene
CC	for HIV-1 that has low functional mutagenicity and is conserved. In
CC	addition, attenuated, non functional vif clones are able to induce
CC	immune responses capable of destroying native pathogen. Vif nucleic
CC	acids may be used to immunize mammals. The attenuated, non-functional
CC	vif genes may be used in concert with other HIV-1 genes to produce
CC	vaccine that has a broad immune response against all viral
CC	components, and which mimics many aspects of the immune responses
CC	induced by a live attenuated virus. Prophylactic vaccines which include
CC	vif could limit both viral escape and contribute to lowering the viral
CC	set point during early infection stages.
XX	
SQ	Sequence 192 AA;
	Query Match 10.9%; Score 77; DB 20; Length 192;
	Best Local Similarity 29.9%; Pred. No. 4;
	Matches 32; Conservative 8; Mismatches 29; Indels 38; Gaps 6;
QY	22 FDMREALLRVKSSERLAMLALAGMGRVLP-----GTGAS-----AIAATVTPKG 69
Db	112 FDCFSASIR-----KAILGHRVSPRCYRAGHSKVSLOYLAI AALITPK- 157
QY	70 ASMKLPPRPQSTKSPBELSKRIEMKNTISQESARVNHRLPEGH 116
Db	158 ---KIRPPLESVRKLTEDR-----WNKPQTKGHRGSHTW-NGH 192
RESULT 20	
AAV01978	
ID	AAV01978 standard; Protein; 192 AA.
AC	AAV01978;
XX	
DT	02-JUL-1999 (first entry)
XX	
DE	HIV-1 viral infectivity factor protein N30.
XX	
KW	Consensus sequence; attenuated; non-functional; accessory protein; vif;
KW	viral infectivity factor; HIV-1; vaccine.
XX	Human immunodeficiency virus type 1.
OS	
XX	WO9913896-A1.
PN	
XX	25-MAR-1999.
PD	

PF 18-SEP-1998; 98WO-US19478.
XX
PR 26-SEP-1997; 97US-0060172.
PR 18-SEP-1997; 97US-0059283.
XX
PA (UYPE-) UNIV PENNSYLVANIA.
XX
PI Ayyavoo V, Nagashunmugam T, Weiner DB;
XX
XX WPI; 1999-263380/22.
DR N-PSDB; AAX35226.
XX
XX New attenuated vif (viral infectivity factor) genes, used in genetic
PT vaccines against HIV-1
XX
XX Claim 2; Fig 7C; 92pp; English.
XX
XX The specification describes novel vif proteins (AAY01969-88) and
CC the genes encoding them (AAX35217-36). The vif gene is an accessory gene
CC for HIV-1 that has low functional mutagenicity and is conserved. In
CC addition, attenuated, non functional vif clones are able to induce
CC immune responses capable of destroying native pathogen. Vif nucleic
CC acids may be used to immunize mammals. The attenuated, non-functional
CC vif genes may be used in concert with other HIV-1 genes to produce
CC vaccine that has a broad immune response against all viral
CC components, and which mimics many aspects of the immune responses
CC induced by a live attenuated virus. Prophylactic vaccines which include
CC vif could limit both viral escape and contribute to lowering the viral
CC set point during early infection stages.
XX
XX Sequence 192 AA;
SQ
Query Match 10.9%; Score 77; DB 20; Length 192;
Best Local Similarity 29.9%; Pred. No. 4;
Matches 32; Conservative 8; Mismatches 29; Indels 38; Gaps 6;
2y 22 FDVVRKALLRVKSSERLALAGMCHRVLP---GTGAS-----AIAATVTPKG 69
Db 112 FDCFSASAIR-----KAILGHRVSPCEYRAGHVKVGLQYLALAIATPK- 157
2y 70 ASMKLKPPRPOSTKSPRLRSKIRENMKTISQESARVNHRLPEGH 116
Db 158 ---KIKPPLPSVRKLTEDR-----WNKPQTKGHRGSHTM-NGH 192
RESULT 21
AAY01970
ID AAY01970 standard; Protein; 192 AA.
XX
AC AAY01970;
XX
DT 02-JUL-1999 (first entry)
XX
DE HIV-1 viral infectivity factor protein N15.
XX
KW Consensus sequence; attenuated; non-functional; accessory protein; vif;
KW viral infectivity factor; HIV-1; vaccine.
XX
CS Human immunodeficiency virus type 1.
XX
EN WO9913896-A1.
XX
FD 25-MAR-1999.
XX
PF 18-SEP-1998; 98WO-US19478.
XX
PR 26-SEP-1997; 97US-0060172.
PR 18-SEP-1997; 97US-0059283.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Ayyavoo V, Nagashunmugam T, Weiner DB;
XX

DR WPI; 1999-263380/22.
DR N-PSDB; AAX35218.
XX
PT New attenuated vif (viral infectivity factor) genes, used in genetic
PT vaccines against HIV-1
XX
XX Claim 2; Fig 7A; 92pp; English.
XX
XX The specification describes novel vif proteins (AAY01969-88) and
CC the genes encoding them (AAX35217-36). The vif gene is an accessory gene
CC for HIV-1 that has low functional mutagenicity and is conserved. In
CC addition, attenuated, non functional vif clones are able to induce
CC immune responses capable of destroying native pathogen. Vif nucleic
CC acids may be used to immunize mammals. The attenuated, non-functional
CC vif genes may be used in concert with other HIV-1 genes to produce
CC vaccine that has a broad immune response against all viral
CC components, and which mimics many aspects of the immune responses
CC induced by a live attenuated virus. Prophylactic vaccines which include
CC vif could limit both viral escape and contribute to lowering the viral
CC set point during early infection stages.
XX
XX Sequence 192 AA;
SQ
Query Match 10.9%; Score 77; DB 20; Length 192;
Best Local Similarity 29.9%; Pred. No. 4;
Matches 32; Conservative 8; Mismatches 29; Indels 38; Gaps 6;
QY 22 FDVVRKALLRVKSSERLALAGMCHRVLP---GTGAS-----AIAATVTPKG 69
Db 112 FDCFSASAIR-----KAILGHRVSPCEYRAGHVKVGLQYLALAIATPK- 157
QY 70 ASMKLKPPRPOSTKSPRLRSKIRENMKTISQESARVNHRLPEGH 116
Db 158 ---KIKPPLPSVRKLTEDR-----WNKPQTKGHRGSHTM-NGH 192
RESULT 22
AAY01971
ID AAY01971 standard; Protein; 192 AA.
XX
AC AAY01971;
XX
DT 02-JUL-1999 (first entry)
XX
DE HIV-1 viral infectivity factor protein N17.
XX
KW Consensus sequence; attenuated; non-functional; accessory protein; vif;
KW viral infectivity factor; HIV-1; vaccine.
XX
OS Human immunodeficiency virus type 1.
XX
PN WO9913896-A1.
XX
PD 25-MAR-1999.
XX
PF 18-SEP-1998; 98WO-US19478.
XX
PR 26-SEP-1997; 97US-0060172.
PR 18-SEP-1997; 97US-0059283.
XX
XX (UYPE-) UNIV PENNSYLVANIA.
XX
XX Ayyavoo V, Nagashunmugam T, Weiner DB;
XX
XX WPI; 1999-263380/22.
DR N-PSDB; AAX35219.
XX
XX New attenuated vif (viral infectivity factor) genes, used in genetic
PT vaccines against HIV-1
XX
XX Claim 2; Fig 7A; 92pp; English.
XX
XX The specification describes novel vif proteins (AAY01969-88) and

CC the genes encoding them (AA35217-36). The vif gene is an accessory gene
CC for HIV-1 that has low functional mutagenicity and is conserved. In
CC addition, attenuated, non functional vif clones are able to induce
CC immune responses capable of destroying native pathogens. Vif nucleic
CC acids may be used to immunize mammals. The attenuated, non-functional
CC vif genes may be used in concert with other HIV-1 genes to produce
CC vaccine that has a broad immune response against all viral
CC components, and which mimics many aspects of the immune responses
CC induced by a live attenuated virus. Prophylactic vaccines which include
CC vif could limit both viral escape and contribute to lowering the viral
CC set point during early infection stages.

XX Sequence 192 AA;
Query Match 10.9%; Score 77; DB 20; Length 192;
Best Local Similarity 29.9%; Pred. No. 4;
Matches 32; Conservative 8; Mismatches 29; Indels 38; Gaps 6;
QY 22 FDMREALLRVKSSERLAMLALAGMCHRVLP-----GTGAS-----AIAATVTPKG 69
Db 112 FDFSESAR-----KALGHVSPRCEYRAGHKVGSLOYLAIALITPK- 157
QY 70 ASMKLPPRPOSTKSPBELRSKIREMKNKTIQSARVNHRLPEGH 116
Db 158 ---KIRPPLPSVRKLTEDR-----WNKPQTKGHRGSHMTM-NGH 192

RESULT 23
AA352172
ID AAY01972 standard; Protein; 192 AA.
XX AAY01972;
DT 02-JUL-1999 (first entry)
DE HIV-1 viral infectivity factor protein N22.
KW Consensus sequence; attenuated; non-functional; accessory protein; vif;
KW viral infectivity factor; HIV-1; vaccine.

OS Human immunodeficiency virus type 1.
XX WO9913896-A1.
XX 25-MAR-1999.
XX 18-SEP-1999; 98WO-US19478.
XX 26-SEP-1997; 97US-0060172.
XX 18-SEP-1997; 97US-0059283.
XX (UYPE-) UNIV PENNSYLVANIA.
XX Ayyavoo V, Nagashumugam T, Weiner DB;
XX WPI; 1999-263380/22.
XX N-PSDB; AAX35220.
PT New attenuated vif (viral infectivity factor) genes, used in genetic
XX vaccines against HIV-1
PS Claim 2; Fig 7B; 92pp; English.

CC The specification describes novel vif proteins (AAY01969-88) and
CC the genes encoding them (AAX35217-36). The vif gene is an accessory gene
CC for HIV-1 that has low functional mutagenicity and is conserved. In
CC addition, attenuated, non functional vif clones are able to induce
CC immune responses capable of destroying native pathogens. Vif nucleic
CC acids may be used to immunize mammals. The attenuated, non-functional
CC vif genes may be used in concert with other HIV-1 genes to produce
CC vaccine that has a broad immune response against all viral
CC components, and which mimics many aspects of the immune responses
CC induced by a live attenuated virus. Prophylactic vaccines which include

CC vif could limit both viral escape and contribute to lowering the viral
CC set point during early infection stages.

XX Sequence 192 AA;
Query Match 10.9%; Score 77; DB 20; Length 192;
Best Local Similarity 29.9%; Pred. No. 4;
Matches 32; Conservative 8; Mismatches 29; Indels 38; Gaps 6;
QY 22 FDMREALLRVKSSERLAMLALAGMCHRVLP-----GTGAS-----AIAATVTPKG 69
Db 112 FDFSESAR-----KALGHVSPRCEYRAGHKVGSLOYLAIALITPK- 157
QY 70 ASMKLPPRPOSTKSPBELRSKIREMKNKTIQSARVNHRLPEGH 116
Db 158 ---KIRPPLPSVRKLTEDR-----WNKPQTKGHRGSHMTM-NGH 192

RESULT 24
AAW89324
ID AAW89324 standard; Protein; 192 AA.
XX AAW89324;
DT 01-JUN-1999 (first entry)
DE HIV-1 P protein sequence.
XX Antigenic composition; primate; lentivirus; nef gene; vaccine;
XX infection; AIDS; HIV-1.
XX Human immunodeficiency virus type 1.
XX US5851813-A.
XX 22-DEC-1998.

XX 27-JAN-1994; 94US-0188583.
XX 27-JAN-1994; 94US-0188583.
XX 12-JUL-1990; 90US-0551945.
XX 09-JUL-1991; 91US-0727494.
XX (HARD) HARVARD COLLEGE.
XX Desrosiers RC;
XX WPI; 1999-080408/07.
XX N-PSDB; AAW81866.
PT Lentivirus antigenic compositions - containing lentivirus with nef
XX gene deletion
XX Disclosure; Fig 2A-R; 93pp; English.

CC The invention relates to an antigenic composition comprising an isolated
CC primate lentivirus whose genome contains an engineered non-revertible
CC null mutation in the nef gene, or an infectious DNA clone in a carrier.
CC The antigenic composition is used in vaccines against infection by the
CC lentivirus, e.g. AIDS.

XX Sequence 192 AA;
Query Match 10.9%; Score 77; DB 20; Length 192;
Best Local Similarity 27.9%; Pred. No. 4;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;
QY 22 FDMREALLRVKSSERLAMLALAG-----MCGHVLPGTGSATATATVTPKGSM 72
Db 112 FDFSESAR-----KALGHVSPRCEYRAGHKVGSLOYLAIALITPK- 157
QY 73 KUKPPRPOSTKSPBELRSKIREMKNKTIQSARVNHRLPEGH 116

Db 158 KIKPPLPSVTKLTEDR-----WPKQTKGHRGSHM-NGH 192

RESULT 25

AA85994

ID AAB85994 standard; Protein; 192 AA.

AC AAB85994;

XX

DT 30-NOV-2001 (first entry)

XX

DE Amino acid sequence of HIV-1 isolate BH10 vif protein.

XX

KW HIV-1; gp120; BH10; vaccine; immunization; vif protein.

XX

OS Human immunodeficiency virus type 1.

XX

PN US6269484-B1.

PD

PD 31-JUL-2001.

XX

PF 30-JUL-1998; 98US-0124900.

XX

PR 07-JUN-1995; 95US-0478536.

PR 19-APR-1995; 95WO-EP01481.

XX

PA (POLY-) POLYMUN SCI IMMUNOBIOLOGISCHE FORSCHUNG.

XX

PI Katinger H, Buchacher A, Ernst W, Ballaun C, Purtscher M;

PI Trkola A, Predl R, Schmatz C, Klima A, Steindl F, Muster T;

XX

DR WPI; 2001-556601/62.

DR N-PSDB; AAB76385.

XX

XX New anti-idiotypic antibodies consisting of one or both amino acid sequences corresponding to amino acid positions 79-84 or 326-400 of the processed gp120 of HIV-isolate BH10, useful as vaccine against HIV-1 infections

PS Claim 1; Columns 29-30; 27pp; English.

XX

CC The invention relates to a peptide fragment comprising of amino acid sequences corresponding to sequences within the processed gp120 of HIV-1 isolate BH10 (GenBank accession M15654). The peptides are useful in the detection, prevention and treatment of HIV-1 infections, and in AIDS therapy. The antibodies are especially useful as vaccines for active and passive immunization, or for the detection and/or determination of HIV-1 infected cells and/or HIV-1 viruses. The present sequence represents the amino acid sequence of a vif protein from HIV-1 isolate BH10 (GenBank accession M15654).

XX

SQ Sequence 192 AA;

Query Match 10.9%; Score 77; DB 22; Length 192;

Best Local Similarity 27.9%; Pred. No. 4;

Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

2y 22 FDMREALLRVKSSERLAMLRLALAG-----KALLGHVSPRCEYQAGHNKVSLOYLALALITPK---- 157

Db 112 FDCFSDSAIR-----KALLGHVSPRCEYQAGHNKVSLOYLALALITPK---- 157

2y 73 KKKPPRQSTKSPRLRLSRKIREMNTISQESARVNHRLPEGH 116

Db 158 KIKPPLPSVTKLTEDR-----WPKQTKGHRGSHM-NGH 192

RESULT 26

AA60421

ID AAP60421 standard; Protein; 203 AA.

AC AAP60421;

XX

DT 25-MAR-2003 (updated)

XX

OS Human T-cell lymphotropic virus.

DT 20-AUG-1991 (first entry)

XX

DE Sequence of LAV virus ORF Q protein.

XX

KW AIDS vaccine; diagnosis; immunoassay; HIV; HTLV-III.

XX

OS Lymphadenopathy virus.

XX

PN WO8602383-A.

XX

PD 24-APR-1986.

XX

PF 18-OCT-1985; 85WO-EP00548.

XX

PR 18-OCT-1984; 84GB-0016013.

PR 16-NOV-1984; 84GB-0029099.

PR 21-JAN-1985; 85GB-0001473.

XX

PA (INSP) INST PASTEUR.

PA (CNRS) CENT NAT RECH SCIENTIF.

XX

PI Montagnier L, Krust B, Chamaret F, Chermann JC, Barresinou F;

PI Alizon M, Sonigo P;

XX

DR WPI; 1986-119166/18.

DR N-PSDB; AAN60365.

XX

PT Purified glycoprotein and peptide(s) - are recognised by sera contg. antibodies against lymphadenopathy virus and useful in detecting AIDS antibodies or in vaccines

XX

PS Disclosure; Fig 4; 75pp; English.

XX

CC The inventors claim a polypeptide which is recognised by sera of human origin contg. antibodies against the virus of lymphadenopathies (LAV) or acquired immune deficiency syndrome (AIDS). Also claimed are various peptides corresp. to the AA sequences deducible from proteins encoded by LAV DNA, defined by CC specific residues (e.g. 12-32, 37-46, 49-79, 88-153) in accordance with a formula given in the specification.

CC (Updated on 25-MAR-2003 to correct PR field.)

CC (Updated on 25-MAR-2003 to correct PA field.)

CC (Updated on 25-MAR-2003 to correct PI field.)

XX

SQ Sequence 203 AA;

Query Match 10.9%; Score 77; DB 7; Length 203;

Best Local Similarity 27.9%; Pred. No. 4.3;

Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

QY 22 FDMREALLRVKSSERLAMLRLALAG-----KALLGHVSPRCEYQAGHNKVSLOYLALALITPK---- 168

Db 123 FDCFSDSAIR-----KALLGHVSPRCEYQAGHNKVSLOYLALALITPK---- 168

QY 73 KKKPPRQSTKSPRLRLSRKIREMNTISQESARVNHRLPEGH 116

Db 169 KIKPPLPSVTKLTEDR-----WPKQTKGHRGSHM-NGH 203

RESULT 27

AA43868

ID AAR43868 standard; Protein; 203 AA.

XX

AC AAR43868;

XX

DT 25-MAR-2003 (updated)

DT 23-DEC-1993 (first entry)

XX

DE HTLV-III SOR gene product (Clone BH10).

XX

KW Polypeptide; antibodies; HTLV; AIDS; vaccine.

XX

OS Human T-cell lymphotropic virus.

```

PR      18-OCT-1985;    85CA-0493377.
PR      03-NOV-1994;    92US-0970954.
PR      17-OCT-1986;    86US-0920119.
PR      01-AUG-1989;    89US-0390499.
PR      06-DEC-1990;    90US-0622278.
PR      20-AUG-1991;    91US-0747506.
PR      01-OCT-1993;    93US-0130565.
PR      06-JUN-1995;    95US-0466920.
PR      05-DEC-1993;    93US-0553109.
PR      28-FEB-1985;    85US-0708562.
PR      30-AUG-1985;    85US-0771230.
PR      30-AUG-1985;    85US-0771247.
PR      30-AUG-1985;    85US-0771248.
XX
XX      (INSP ) INST PASTEUR.
XX      (CNRS ) CENT NAT RECH SCI.
PA
PA      Montangniet L, Krust B, Chanaret S, Clavel F, Chermann J;
PI      Barre-sinoussi F, Alizon M, Sonigo P, Cole S, Danos O;
PI      Wain-Hobson S;
XX
XX      WPI; 2002-711525/77.
DR      N-PSDB; AAL49920.
XX
XX      Novel chemically synthesized Human Immunodeficiency Virus envelope
PT      protein, useful in vitro diagnostic method for the detection of the
PT      presence or absence of antibodies that bind to antigens of HIV-1
PT      retrovirus .
XX
XX      Disclosure; Fig 3; 3lpp; English.
XX
XX      The present invention relates to a chemically synthesised env peptide of
CC      Human Immunodeficiency Virus (HIV) of less than 150 amino acid residues.
CC      Such a peptide is useful in an in vitro diagnostic method for the
CC      detection of the presence or absence of antibodies that bind to antigens
CC      of HIV-1 retrovirus, by contacting the peptide with a biological fluid
CC      for a time and under conditions sufficient for the peptide and antibody
CC      in the biological fluid to form a peptide-antibody complex, detecting the
CC      formation of the peptide-antibody complex by comparing the formation of
CC      peptide-antibody complex formation with a control sample, where the
CC      formation of peptide-antibody complex is correlated with the presence of
CC      antibodies that bind to antigens of HIV-1 retrovirus in the biological
CC      sample. It can also be used for preparation of vaccine compositions
CC      against AIDS or related syndromes. The present sequence is the
CC      lymphadenopathy-associated virus LAV ORF Q protein. The LAV virus was
CC      isolated from a patient with AIDS.
XX
XX      Sequence 203 AA;
SQ
Query Match          10.9%; Score 77; DB 23; Length 203;
Best Local Similarity 27.9%; Pred. No. 4.3;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;
QY      22 FDVMREALLRVKSSERLAMLRLAAG-----MCGHRVLPGTGASAIATVTGKASM 72
       ||| : : : ||| : : : ||| : : : ||| : : : |||
Db      123 FDCFSDSAIR-----KALLGHIVSPCEYQAGHKVGSYLQYLAALAITPK---- 168
QY      73 KLKPPRPOSTKSPELRELRSKIREKNKTISQESARVNHLPEGH 116
       ||| : : : ||| : : : ||| : : : ||| : : : |||
Db      169 KIKPLPVSVKLTEDR-----WNKPQKTKGHRGSHTM-NGH 203
XX
XX      RESULT 29
XX      ID AAB63854
XX      ID AAB63854 standard; Protein; 214 AA.
XX      AAC AAB63854;
XX
XX      DT 26-MAR-2001 (first entry)
XX
XX      DE HUMAN prostate cancer associated antigen protein sequence SEQ ID NO:1216.
XX      KW Human; breast cancer; gastric cancer; prostate cancer; diagnosis;

```


KM cancer associated antigen; cytostatic; cancer vaccine.
XX Homo sapiens.
OS
XX WO200073801-A2.
XX
XX PD 07-DEC-2000.
XX
XX PF 26-MAY-2000; 2000WO-US14749.
XX
XX PR 28-MAY-1999; 99US-0136526.
XX PR 10-SEP-1999; 99US-0153454.
XX
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX
XX PI Obata Y;
XX
XX DR WPI; 2001-025274/03.
XX
XX Nucleic acids encoding breast, gastric and prostate cancer associated
PT antigen precursors, useful for diagnosing and treating a condition
PT characterized by expression of an abnormal amount of a protein, e.g.
PT cancer -
XX
XX PS Example 1; Page 747-748; 799pp; English.
XX
XX CC AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
CC represent nucleotide sequences encoding human breast, gastric and
CC prostate cancer associated antigen precursors (CAAP) respectively.
CC AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
CC represent human breast, gastric and prostate CAAP protein sequence
CC respectively. CAAPs have cytostatic activity and can be used in the
CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic
CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
CC condition characterised by expression of an abnormal amount of a protein,
CC e.g. cancer.
XX
XX SQ Sequence 214 AA;
Query Match 10.8%; Score 76.5; DB 22; Length 214;
Best Local Similarity 26.1%; Pred. No. 5.2;
Matches 36; Conservative 17; Mismatches 44; Indels 41; Gaps 6;
QY 20 BTDFVMEALLRVKSSERLAVLRA-----LAGMCGHVRVLPQTG-----ASAIA 62
Db 30 EQLDAINKELRLQEEKESTELRAEETENRVASVSLGLENLARVHPGTSITASVTASSLA 89
QY 63 ATVTPKGASM-KLKPPRPQ-----STKSPELRELSRKI-----RENNKTIISOESA 106
Db 90 SSSPPSGHSTFKLTPRSPAREMDRMGVMTLPDSXKXKRRKIADVVEEDGREDKATIKCETS 149
QY 107 -----RVNHRLPQGH 116
Db 150 PPPTPRALRMTHLPSSY 167
RESULT 30
ID AAY50122 standard; Protein; 373 AA.
XX
XX AC AAY50122;
XX
XX DT 09-FEB-2000 (first entry)
XX
XX DE Human histone fusion protein HHFP.
XX
XX CW Human histone fusion protein; HHFP; nucleosome; basic; histone; H2A;
CW H1; nonhistone protein; DNA binding; leucine zipper; mH2A;
CW transcription regulation; diagnosis; prevention; treatment;
CW proliferative disorder; cancer; inflammatory disorder; asthma;
CW multiple sclerosis; AIDS.
XX
XX JS Homo sapiens.

XX Key Location/Qualifiers
FH Modified-site 2..4
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 7..10
FT /note= "cAMP/cGMP-dependent protein kinase
FT phosphorylation site"
FT Modified-site 8..11
FT /note= "cAMP/cGMP-dependent protein kinase
FT phosphorylation site"
FT Modified-site 10..12
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 13..15
FT /note= "Thr is O-phosphorylated by protein kinase C"
FT Modified-site 16..18
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 16..18
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 77..79
FT /note= "Thr is O-phosphorylated by protein kinase C"
FT Modified-site 117..120
FT /note= "cAMP/cGMP-dependent protein kinase
FT phosphorylation site"
FT Binding-site 133..161
FT /note= "Highly basic DNA binding region"
FT Modified-site 140..142
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 146..148
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 158..160
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Domain 183..213
FT /note= "Leucine zipper"
FT Modified-site 188..190
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 220..223
FT /note= "Thr is O-phosphorylated by casein kinase II"
FT Modified-site 294..296
FT /note= "Thr is O-phosphorylated by protein kinase C"
FT Modified-site 317..319
FT /note= "Ser is O-phosphorylated by protein kinase C"
FT Modified-site 346..348
FT /note= "Ser is O-phosphorylated by protein kinase C"
XX US981221-A.
XX 09-NOV-1999.
XX 26-MAR-1997; 97US-0824878.
XX 26-MAR-1997; 97US-0824878.
XX (INCY-) INCYTE PHARM INC.
XX Hillman JL, Goli SK;
XX WPI; 1999-833314/54.
XX N-PSDB; AAZ32676.
XX Nucleic acids encoding histone fusion proteins useful for the
PT prevention, diagnosis and treatment of disorders associated with cell
PT proliferation and inflammation -
XX
XX PS Claim 1; Fig 1; 29pp; English.
XX
XX CC This sequence represents human histone fusion protein HHFP. Nucleic
CC acids encoding HHFP were first identified in a human breast tissue
CC cDNA library and this sequence represents a consensus. HHFP is a
CC naturally occurring protein which contains regions homologous with both
CC histones and nonhistone proteins. The N-terminus of HHFP resemble the
CC full-length human histone H2A, while residues 133-161 are highly basic
CC and have similarity with the C-terminus of histone H1, indicating that
CC HHFP has DNA binding potential. There is a leucine zipper region in the

CC nonhistone region of HHFP (between residues 183 and 213) indicating a
 CC potential transcription-regulating function. HHFP has structural and
 CC functional homology with mH2A, a rat histone-nonhistone fusion protein
 CC identified in rat liver nucleosomes. HHFP and nucleotides encoding it
 CC may be used in the diagnosis, prevention and treatment of disorders
 CC associated with cell proliferation (especially cancers) and inflammation
 CC (e.g. AIDS, asthma and multiple sclerosis). They may also be used to
 CC produce and identify modulators of histone function which may be used to
 CC downregulate histone activity and therefore reduce rates of cell
 CC proliferation and reduce inflammatory reactions.
 XX
 SQ Sequence 373 AA;
 Query Match 10.8%; Score 76.5; DB 20; Length 373;
 Best Local Similarity 23.3%; Pred. No. 11;
 Matches 31; Conservative 20; Mismatches 61; Indels 21; Gaps 3;
 QY 26 REALLRVKSSERLAMRLALAGMCHRVLPOTGASATAIAATVTPKGSMKJK-PPRPQS 81
 DB 79 RHLLAVANDEELNQLKGVLTASGGVLPNIHPELLA---KKRGSGKLEAIITPPPAKK 135
 QY 82 TKSP-----LRELSRKIREMNKTIQESARVNHRLPEGHPLLEKRAEYFR 127
 DB 136 AKSPSQKPVSKKAGGKKGARKKKQGEVSKAASADSNNGEHLDPDGTVLSTKSLFLG 195
 QY 128 HLRLSKSQGVNRL 140
 DB 196 QKLNLIHSEISNL 208
 RESULT 31
 AAB30626
 ID AAB30626 standard; Protein; 373 AA.
 XX
 AC AAB30626;
 XX
 DT 19-NAR-2001 (first entry)
 XX
 DE Amino acid sequence of a human histone fusion protein (HFP).
 XX
 KW Human; histone fusion protein; HFP; DNA conformational change; leukaemia;
 KW incyte clone 2297753; cell proliferation disorder; sarcoma; lymphoma;
 KW cancer; inflammation; allergy; asthma; bronchitis; lupus erythematosus;
 KW multiple sclerosis; thyroiditis.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 2..4
 FT /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 7..10
 FT /note= "potential CAMP- and cGMP-dependent protein
 FT kinase phosphorylation site"
 FT Modified-site 8..11
 FT /note= "potential CAMP- and cGMP-dependent protein
 FT kinase phosphorylation site"
 FT Modified-site 10..12
 FT /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 13..15
 FT /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 16..18
 FT /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 77..79
 FT /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 117..120
 FT /note= "potential CAMP- and cGMP-dependent protein
 FT kinase phosphorylation site"
 FT Modified-site 140..142
 FT /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 146..148
 FT /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 158..160
 FT /note= "potential protein kinase C phosphorylation site"

FT Region 183..213
 FT /note= "leucine zipper region"
 FT Modified-site 188..190
 FT /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 220..223
 FT /note= "potential casein kinase phosphorylation site"
 FT Modified-site 294..296
 FT /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 317..319
 FT /note= "potential protein kinase C phosphorylation site"
 FT Modified-site 346..348
 FT /note= "potential protein kinase C phosphorylation site"
 XX
 PN US6136314-A.
 XX
 PD 24-OCT-2000.
 XX
 PF 14-JUL-1999; 99US-0353688.
 XX
 PR 26-MAR-1997; 97US-0824878.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Hillman JL, Goli SK;
 XX
 DR WPI; 2001-023156/03.
 DR N-PSDB; RAC62360.
 XX
 PT Novel human histone fusion protein, useful for diagnosing, preventing
 PT or treating disorders associated with cell proliferation (e.g. bone
 PT cancer or leukaemia) or inflammation (e.g. bronchitis or thyroiditis)
 XX
 PS Claim 1; Fig 1A-E; 29pp; English.
 XX
 CC The present sequence represents a human histone fusion protein (HFP).
 CC The protein regulates the conformational changes of DNA. HFP nucleic
 CC acids were first identified in incyte clone 2297753 from a breast
 CC tissue cDNA library. HFP is useful for diagnosing, preventing or
 CC treating disorders associated with cell proliferation (e.g. sarcoma,
 CC lymphoma, leukaemia, or bone, colon or brain cancer) and inflammation
 CC (e.g. allergies, asthma, bronchitis, lupus erythematosus, multiple
 CC sclerosis or thyroiditis).
 XX
 SQ Sequence 373 AA;

Query Match 10.8%; Score 76.5; DB 22; Length 373;
 Best Local Similarity 23.3%; Pred. No. 11;
 Matches 31; Conservative 20; Mismatches 61; Indels 21; Gaps 3;
 QY 26 REALLRVKSSERLAMRLALAGMCHRVLPOTGASATAIAATVTPKGSMKJK-PPRPQS 81
 DB 79 RHLLAVANDEELNQLKGVLTASGGVLPNIHPELLA---KKRGSGKLEAIITPPPAKK 135
 QY 82 TKSP-----LRELSRKIREMNKTIQESARVNHRLPEGHPLLEKRAEYFR 127
 DB 136 AKSPSQKPVSKKAGGKKGARKKKQGEVSKAASADSNNGEHLDPDGTVLSTKSLFLG 195
 QY 128 HLRLSKSQGVNRL 140
 DB 196 QKLNLIHSEISNL 208
 RESULT 32
 AAM79480
 ID AAM79480 standard; Protein; 1778 AA.
 AC AAM79480;
 XX
 XX 06-NOV-2001 (first entry)
 XX
 DE Human protein SEQ ID NO 3126.
 XX
 KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 OS Homo sapiens.
 XX WO200157130-A2.
 PN 09-AUG-2001.
 PD 05-FEB-2001; 2001WO-US04098.
 PF 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI; 2001-476283/51.
 DR N-PSDB; AAK52613.
 XX Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX Claim 20; Page 258-259; 6221pp; English.
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAW80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX Sequence 1778 AA;
 SQ Query Match 10.8%; Score 76.5; DB 22; Length 1778;
 Best Local Similarity 29.7%; Pred. No. 79;
 Matches 35; Conservative 13; Mismatches 45; Indels 25; Gaps 4;
 QY 3 STSTTTNFVAENRPTFGTDFVMEALLRVKSSERLALAGMCGHRLVPGTGASAI 62
 DB 507 SPRTTENTLERKP-----YSPRDSLPALTSSALAFKLS-----RSKLL 547
 QY 63 ATVTGKASMLKPPRPOSTKSPPELRELSRKIRENNKTISOESARVNHRLPEGHPLLE 120
 DB 548 ATVACLGASPLKVKSKP-SLSWKELRG-----RREVPLAEQVARECEERLLQFPPLFE 599
 RESULT 33
 ID AAW78496
 XX AAW78496 standard; Protein; 2099 AA.
 AC AAW78496;
 XX 06-NOV-2001 (first entry)
 DT
 XX

DE Human protein SEQ ID NO 1158.
 XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.
 XX Homo sapiens.
 OS WO200157190-A2.
 PN 09-AUG-2001.
 PD 05-FEB-2001; 2001WO-US04098.
 PF 03-FEB-2000; 2000US-0496914.
 PR 27-APR-2000; 2000US-0560875.
 PR 20-JUN-2000; 2000US-0598075.
 PR 19-JUL-2000; 2000US-0620325.
 PR 01-SEP-2000; 2000US-0654936.
 PR 15-SEP-2000; 2000US-0663561.
 PR 20-OCT-2000; 2000US-0693325.
 PR 30-NOV-2000; 2000US-0728422.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI; 2001-476283/51.
 DR N-PSDB; AAK51629.
 XX Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX Claim 20; Page 3392-3396; 6221pp; English.
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAW78323-AAW80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAW80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX Sequence 2099 AA;
 SQ Query Match 10.8%; Score 76.5; DB 22; Length 2099;
 Best Local Similarity 29.7%; Pred. No. 97;
 Matches 35; Conservative 13; Mismatches 45; Indels 25; Gaps 4;
 QY 3 STSTTTNFVAENRPTFGTDFVMEALLRVKSSERLALAGMCGHRLVPGTGASAI 62
 DB 835 SPRTTENTLERKP-----YSPRDSLPALTSSALAFKLS-----RSKLL 875
 QY 63 ATVTGKASMLKPPRPOSTKSPPELRELSRKIRENNKTISOESARVNHRLPEGHPLLE 120
 DB 876 ATVACLGASPLKVKSKP-SLSWKELRG-----RREVPLAEQVARECEERLLQFPPLFE 927
 RESULT 34
 ID AAR43876
 XX AAR43876 standard; Protein; 203 AA.
 AC AAR43876;

XX 25-MAR-2003 (updated)
DT 23-DEC-1993 (first entry)
XX DE HTLV-III SOR gene product (Clone BH5).
XX KW Polypeptide; antibodies; HTLV; AIDS; vaccine.
XX OS Human T-cell lymphotropic virus.
XX PN EP552850-A1.
XX PD 28-JUL-1993.
XX PF 10-OCT-1985; 93EP-0200929.
XX PR 10-OCT-1984; 84US-0659339.
XX PR 23-JAN-1985; 85US-0693866.
XX PR 10-OCT-1985; 85EP-0307260.
XX (CENZ) CENTOCOR INC.
XX PI Chang NT, Gallo RC, Wong-staal F;
XX WPI; 1993-236543/30.
XX N-PSDB; AAQ45921.
XX Cloning and expression of new HTLV-III DNA - used to obtain
PT polypeptide(s) and antibodies for diagnosis, prevention and
PT treatment of HTLV-III infection, partic. AIDS
XX Disclosure; Figure 3; 31pp; English.
XX A fragment of DNA approximately 200-500 base pairs in length is
CC ligated into a vector and used to transform E.coli. These cells then
CC express a polypeptide which is immunoreactive with HTLV-III-specific
CC antibody. The HTLV-III polypeptides can be used for the production
CC of antibodies in immunoassays for the detection of HTLV-
CC III-specific antibodies and in vaccines for the prevention of AIDS.
CC The antibodies can also be used to detect HTLV-III polypeptides.
CC (Updated on 25-MAR-2003 to correct PN field.)
CC (Updated on 25-MAR-2003 to correct PF field.)
XX Sequence 203 AA;
Query Match 10.7%; Score 76; DB 14; Length 203;
Best Local Similarity 27.9%; Pred. No. 5.5;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;
QY 22 FDVMEALLRVKSSERLAMLRLAG-----MCGHRLVPGTGASAIATVTPKQASM 72
Db 123 FDCFSDSAIR-----KALLGHIVSPCEYQAGHNKVGSLQYLALALITPK---- 169
QY 73 KUKPRPOSTKGPRLSRKIRENNKTIISOESARVNHRLPEGH 116
Db 169 KVKPPLPSVTKLTEDR-----WNKPKQTKGHRGSHTM-NGH 203
RESULT 35
AAB63752
ID AAB63752 standard; Protein; 259 AA.
XX AC AAB63752;
XX DT 26-MAR-2001 (first entry)
XX DE Human prostate cancer associated antigen protein sequence SEQ ID NO:1114.
XX KW Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
XX cancer associated antigen; cytostatic; cancer vaccine.
XX OS Homo sapiens.

XX WO2000073801-A2.
XX PD 07-DEC-2000.
XX PF 26-MAY-2000; 2000WO-US14749.
XX PR 28-MAY-1999; 99US-0136526.
XX PR 10-SEP-1999; 99US-0153454.
XX PA (LUDW-) LUDWIG INST CANCER RES.
XX PI Obata Y;
XX WPI; 2001-025274/03.
XX Nucleic acids encoding breast, gastric and prostate cancer associated
PT antigen precursors, useful for diagnosing and treating a condition
PT characterized by expression of an abnormal amount of a protein, e.g.
PT cancer -
XX Example 1; Page 701; 799pp; English.
XX AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
CC represent nucleotide sequences encoding human breast, gastric and
CC prostate cancer associated antigen precursors (CAAP) respectively.
CC AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
CC represent human breast, gastric and prostate CAAP protein sequence
CC respectively. CAAPs have cytostatic activity and can be used in the
CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic
CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
CC condition characterised by expression of an abnormal amount of a protein,
CC e.g. cancer.
XX SQ Sequence 259 AA;
Query Match 10.7%; Score 76; DB 22; Length 259;
Best Local Similarity 20.9%; Pred. No. 7.5;
Matches 31; Conservative 27; Mismatches 76; Indels 14; Gaps 2;
QY 4 TSTTTFVANRRPTFGETPDVMEALLRVKSSERLAMLRLAGMCGHRLVPGTGASAI 63
Db 2 TQFTQYWAQREADFKEITLQERE-ILENAERRLAIFDLVGVKCDTREAAKDCAIKV 60
QY 64 TVTFKASMKLKPFPQSTKSPRLSRKIRENNKTIISOESARV-----NH 110
Db 61 ETBEATACLEKFNQIKAEIAKTKGELIKTELKRENESSLIQELETSNKKIITNQ 120
QY 111 RLPEGHPLLEKRAEYFRHLRLSLKSGQVN 138
Db 121 RIKELINIIDQKEDTINEFONLASHMEN 148
RESULT 36
AAB68120
ID ABB68120 standard; Protein; 442 AA.
XX AC ABB68120;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 31152.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.
XX 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX N-PSDB; ABL12223.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX Disclosure; SEQ ID NO 31152; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABBS7737-ABBS72072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 442 AA;
Query Match 10.7%; Score 75.5; DB 22; Length 442;
Best Local Similarity 21.8%; Pred. No. 17;
Matches 33; Conservative 21; Mismatches 42; Indels 57; Gaps 6;
Y 34 SSERLAMLALAGMCG-----HRVLPQTGA-----SAIAATV 65
b 287 SNQEPATPTSLAGCGVNVILDDQPRSPVGPAGSSKAINGFGSLSLISTPAATAPV 346
Y 66 TPKGASMKLPPRPQSTKPELRELS-----RKIRE-----MNKT 100
b 347 TPAGATLDDVPPPMQTS--LNSISADGDTQAKKVTCSGTQGYSTIDFIRTVLNKS 404
Y 101 IQESARVNHRLPEGHPLLEKRAEYFRHLRLSLK 133
b 405 STELPETVTHRQSHSHDAELRIT--RHSKCIR 435
RESULT 37
BG19829
D ABG19829 standard; Protein; 542 AA.
X ABG19829;
X 13-FEB-2002 (first entry)
X Novel human diagnostic protein #19820.
X Human; chromosome mapping; gene mapping; gene therapy; forensic;
X food supplement; medical imaging; diagnostic; genetic disorder.
X Homo sapiens.
X WO200175067-A2.
X 11-OCT-2001.
X 30-MAR-2001; 2001WO-US08631.
X 31-MAR-2000; 2000US-0540217.
X 23-AUG-2000; 2000US-0649167.
X (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;
XX WPI; 2001-639362/73.
XX N-PSDB; AAS84016.
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX Claim 20; SEQ ID No 50188; 103pp; English.
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 542 AA;
Query Match 10.7%; Score 75.5; DB 22; Length 542;
Best Local Similarity 23.7%; Pred. No. 22;
Matches 31; Conservative 18; Mismatches 53; Indels 29; Gaps 4;
QY 9 NFVAENRPTFCETEDVMREALRVKSSERLAMLRLALAGMCGHRVLPQTGASAIATVT-- 66
Db 235 NLLILKKPVF-----LKPKRLLHLRPSLECCCPMMIKGASMSRDIKFTPL 281
QY 67 --PKGASMKLPPRPQSTKPELRELSRKIREMNKTISQESARVNHRLPEGHPLLEKR-- 122
Db 282 PSRAASDRLMEPKGKGLAEALKKQLNSIQESTQAFDEHLKR-----LFERRVK 331
QY 123 AEYFRHLRLSLK 133
Db 332 AEMVTNQEELK 342
RESULT 38
ABJ19818
ID ABJ19818 standard; Protein; 1257 AA.
XX ABJ19818;
XX 10-APR-2003 (first entry)
XX Androgen-independent prostate cancer-related protein - SEQ ID No 51.
XX Androgen-independent cancer; androgen ablation therapy; prostate cancer;
XX androgen-dependent prostate cancer; prostate cancer.
XX Unidentified.
XX WO200298358-A2.
XX 12-DEC-2002.

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PR 04-JUN-2002; 2002WO-US17594.
XX
PR 04-JUN-2001; 2001US-295917P.
PR 13-NOV-2001; 2001US-350666P.
PR 29-MAR-2002; 2002US-368689P.
PR 12-APR-2002; 2002US-372246P.
PR 31-MAY-2002; 2002US-0160233.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar DEH, Agus D, Mack DH;
XX
DR WPI; 2003-148602/14.
XX
PT Detecting an androgen-independent prostate cancer cell in a sample or
PT diagnosing androgen-dependent prostate cancer, by determining the
PT presence or absence of genes whose expressions are up- or
PT down-regulated -
XX
PS Claim 1; Page 203; 210pp; English.
XX
CC The invention comprises a method for detecting an androgen-independent
CC cancer cell in a sample from a patient who has undergone androgen
CC ablation therapy. The method involves determining the presence or absence
CC of nucleic acids that are either up-regulated or down-regulated in
CC prostate cancer. The method is useful for detecting an androgen-
CC independent prostate cancer cell in a sample from a patient who has
CC undergone androgen ablation therapy. The method is particularly useful
CC for diagnosing androgen-dependent prostate cancer, prostate cancer
CC undergoing androgen withdrawal, or androgen-independent prostate cancer.
CC The present amino acid sequence represents a protein which is encoded by
CC a gene that is either up-regulated or down-regulated in prostate cancer.
XX
SQ Sequence 1257 AA;

Query Match 10.7%; Score 75.5; DB 24; Length 1257;
Best Local Similarity 26.1%; Pred. No. 65;
Matches 36; Conservative 17; Mismatches 44; Indels 41; Gaps 6;

2Y 20 BTDFVMEALLRVKSSERLAMLRA-----LAGMCGHRVLPQTG-----ASAIA 62
Db 655 EQLDAINKEIRLIOEKESTELRAEEIENRVASVLEGLNLMVHPTSTASVTASSLA 714

2Y 63 ATVTPKGASM-KLAPPRQ-----STKSPELRELSRKI-----RENNKTIQOESA 106
Db 715 SSSPPSGHSTPKLTPRFPAREMDRMGMVTLPSDLRKRRKRIAVVEEDGREDKATIKETS 774

2Y 107 -----RVNHRLEPEGH 116
Db 775 PPPTFRALRWHTHTLPSSY 792

RESULT 39
ABB62927
ID ABB62927 standard; Protein; 476 AA.
XX
AC ABB62927;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 15573.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.

PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
DR N-PSDB; ABL07030.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Disclosure; SEQ ID NO 15573; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 476 AA;

Query Match 10.6%; Score 75; DB 22; Length 476;
Best Local Similarity 21.0%; Pred. No. 21;
Matches 29; Conservative 28; Mismatches 55; Indels 26; Gaps 5;

QY 11 VAEINPTFGTETDVMREALLR----VKSSERLAMLRLAGMCGHRVLPQTGASAIATVT 66
Db 139 LAQNRTLAGDV-DMLKTLVRLNVQIESYQDQRLGEGAPTGC-----GSTKYSSSSA 190

QY 67 PKGASKMLKPPRPQSTKSPLELSRKIREMKNTISQESARVNH-----RLPECHPLL 119
Db 191 P-----YPPILPTTLGLLQAYDESURDKDALLAQYNTFEHFTGTGELKRALEENTKLL 243

QY 120 EKRAEYFRHLRSKSGV 137
Db 244 QSQEQLRRLDGLGWREERV 261

RESULT 40
ABB68597
ID ABB68597 standard; Protein; 1116 AA.
XX
AC ABB68597;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 32583.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE ) PE CORP NY.

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PI Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
DR N-PSDB; ABL12700.
XX
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions -
XX
XX
XX Disclosure; SEQ ID NO 32583; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
sequences (ABL01840-ABL16175) and the encoded proteins
(ABB57737-ABB72072).
XX The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1116 AA;
3Q
Query Match 10.5%; Score 74.5; DB 22; Length 1116;
Best Local Similarity 29.2%; Pred. No. 71;
Matches 49; Conservative 19; Mismatches 55; Indels 45; Gaps 10;
2Y 1 MESTSTTNFVAENRPTFGETFDMREALLRVKSSERLALMRLAGMCGHRVLPGTGASA 60
3b 747 MASTSTS-----RQSPCAT---PRAGLSRKNSCSTFSVNLGLAGMLNERGIKAVTPSA 797
2Y 61 I-----AATVTPKGAMKLPKPQSTKSPELRELS-----RKI-----REMNK 99
3b 798 LNTPAGEFNFSPTVPCN-SPEGSPRAQSP-PLFGLLSCGADLIRKIVGDQHQOQOQK 855
2Y 100 TISQESARVNRHLPDEGHPLLEKRAEYFRHLRSL-----XSQGVNRLI 141
3b 856 QRSLSKQOQOQKIMLSH--LERRA-----LRSLNLIEKVESIGLENII 896

Search completed: November 14, 2003, 10:40:16
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: November 14, 2003, 10:38:35 ; Search time 21 Seconds
(without alignments)
284.087 Million cell updates/sec

Title: US-10-087-573-2
Perfect score: 708
Sequence: 1 MESTSTTTFVFAENRPTFGE.....RAEYFRHLRLSKSQGVNRLI 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pdp.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pdp.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pdp.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pdp.*
- 5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pdp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	81.5	11.5	1419	US-09-252-991A-31822	Sequence 31822, A
2	80	11.3	473	US-09-252-991A-31406	Sequence 31406, A
3	78	11.0	686	US-09-107-532A-5002	Sequence 5002, Ap
4	77	10.9	192	US-09-124-900-4	Sequence 4, Appli
5	77	10.9	203	US-08-463-210-10	Sequence 10, Appl
6	76.5	10.8	373	US-08-824-878-1	Sequence 1, Appli
7	76.5	10.8	373	US-09-353-688-1	Sequence 1, Appli
8	76.5	10.8	501	US-09-252-991A-23033	Sequence 23033, A
9	75.5	10.7	741	US-09-252-991A-30333	Sequence 30333, A
10	74	10.5	231	US-09-252-991A-32190	Sequence 32190, A
11	74	10.5	383	US-09-252-991A-27087	Sequence 27087, A
12	72.5	10.2	248	US-09-252-991A-32808	Sequence 32808, A
13	72.5	10.2	342	US-08-911-853-2	Sequence 2, Appli
14	72.5	10.2	342	US-09-479-409-2	Sequence 2, Appli
15	72.5	10.1	282	US-09-479-453-2	Sequence 2, Appli
16	71.5	10.1	282	US-09-252-991A-26169	Sequence 26169, A
17	71.5	10.1	976	US-08-894-997-50	Sequence 50, Appl
18	71.5	10.1	2293	US-09-369-590-2	Sequence 2, Appli
19	71	10.0	558	US-09-252-991A-26115	Sequence 26115, A
20	70.5	10.0	329	US-09-252-991A-30436	Sequence 30436, A
21	70.5	10.0	954	US-09-251-645-12	Sequence 12, Appl
22	70	9.9	185	US-09-252-991A-24804	Sequence 24804, A
23	70	9.9	242	US-09-252-991A-19038	Sequence 19038, A
24	70	9.9	443	US-08-793-475-6	Sequence 6, Appli
25	69.5	9.8	296	US-09-252-991A-23961	Sequence 23961, A
26	69.5	9.8	354	US-08-216-894-4	Sequence 4, Appli
27	69.5	9.8	354	US-09-115-746-4	Sequence 4, Appli

28	69.5	9.8	564	2	US-08-216-894-2	Sequence 2, Appli
29	69.5	9.8	564	3	US-09-115-746-2	Sequence 2, Appli
30	69.5	9.8	643	2	US-08-216-894-8	Sequence 8, Appli
31	69.5	9.8	643	3	US-09-115-746-8	Sequence 8, Appli
32	69.5	9.8	671	4	US-09-252-991A-19375	Sequence 19375, A
33	69	9.7	232	4	US-09-252-991A-30831	Sequence 30831, A
34	69	9.7	411	4	US-09-252-991A-25526	Sequence 25526, A
35	69	9.7	454	4	US-09-252-991A-24836	Sequence 24836, A
36	69	9.7	461	4	US-09-252-991A-32102	Sequence 32102, A
37	69	9.7	553	3	US-09-413-814-3	Sequence 3, Appli
38	69	9.7	834	1	US-07-977-434-8	Sequence 8, Appli
39	69	9.7	834	1	US-08-458-819-8	Sequence 8, Appli
40	69	9.7	834	5	FCU-US91-07035-8	Sequence 8, Appli
41	69	9.7	1064	4	US-09-252-991A-17508	Sequence 17508, A
42	68.5	9.7	371	4	US-09-252-991A-32348	Sequence 32348, A
43	68.5	9.7	408	4	US-09-252-991A-21775	Sequence 21775, A
44	68.5	9.7	600	4	US-09-134-001C-5293	Sequence 5293, Ap
45	68	9.6	155	4	US-09-252-991A-18135	Sequence 18135, A

ALIGNMENTS

RESULT 1
US-09-252-991A-31822
; Sequence 31822, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31822
; LENGTH: 1419
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31822

Query Match 11.5%; Score 81.5; DB 4; Length 1419;
Best Local Similarity 28.5%; Pred. No. 3.7; Mismatches 13; Gaps 5;
Matches 35; Conservative 16;
QY 25 MREALLRVKSSER-LA----MLRALAGMCHRYLPQTGASATAATVTPKGASMKLKP RP 79
Db 881 LREQLLRARELDQLADTGELEALLAGLAGRFVAFQPGGDPINPQVPSGRNLF AF----- 936
QY 80 QSTKSPSELRELGRKIREMKNKTSQESARVNH--RLPEGHPLLEKRAEYFRHLRLSKSQGV 137
Db 937 EADKVPTRAAEAGAEAFQQLL--ESYRAEHQGRAPEKLAFLSWSETMRHLGIVESQAL 994
QY 138 NRL 140
Db 995 HAL 997

RESULT 2
US-09-252-991A-31406
; Sequence 31406, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31406
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31406

Query Match 11.3%; Score 80; DB 4; Length 473;
Best Local Similarity 27.5%; Pred. No. 1.2;
Matches 36; Conservative 17; Mismatches 46; Indels 32; Gaps 7;

Qy 20 EFDVNMREALLRVKSSERLAMLRLAGMCGHRVLPCTGASATAATVTPKG-ASMKLK--- 75
Db 287 EYDPLSRRLFLYLKCEKNPWAQALV-----RFAQGPQQAIV---VTRSGFVAQKIQAVQ 338
Qy 76 -PPRPOSTKSPBELRSKIREMNTKISOESARVNHRLPEGHPLLEKRA-----EYF 126
Db 339 IAPRPQ--MPAERYKLAEQARLT-----VNFRTQEGSALLDNKALLDVQRLLDYL 387
Qy 127 RHLRSLSKQGV 137
Db 388 RQNRKLQERTV 398

RESULT 3
US-09-107-532A-5002
; Sequence 5002, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Denke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5002:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 686 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...686
; SEQUENCE DESCRIPTION: SEQ ID NO: 5002:
US-09-107-532A-5002

Query Match 11.0%; Score 78; DB 4; Length 686;
Best Local Similarity 38.9%; Pred. No. 3.4;
Matches 21; Conservative 8; Mismatches 13; Indels 12; Gaps 2;

Qy 61 IAAVTPKASMKLKPPRPOSTKSPBELRSKIREMNTKISOESARVNHRLPE 114
Db 544 MAHAVSPGT-----KVKQTRSLRLARISRKISESNTKIRQEA-----HLAPQ 585

RESULT 4
US-09-124-900-4
; Sequence 4, Application US/09124900
; Patent No. 6268484
; GENERAL INFORMATION:
; APPLICANT: KATINGER, Hermann
; APPLICANT: BUCHACHER, Andrea
; APPLICANT: ERNST, Wolfgang
; APPLICANT: BALLAUN, Claudia
; APPLICANT: FURTSCHER, Martin
; APPLICANT: TRKOLA, Alexandra
; APPLICANT: PREDL, Renate
; APPLICANT: SCHMATZ, Christine
; APPLICANT: KLIMA, Annelies
; APPLICANT: STEINDL, Franz
; APPLICANT: MUSTER, Thomas
; TITLE OF INVENTION: HIV-Vaccines
; FILE REFERENCE: 1939-112P
; CURRENT APPLICATION NUMBER: US/09/124,900
; CURRENT FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: PCT/EP95/01481
; PRIOR FILING DATE: 1995-04-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-124-900-4

Query Match 10.9%; Score 77; DB 3; Length 192;
Best Local Similarity 27.9%; Pred. No. 0.76;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

Qy 22 FDMREALLRVKSSERLAMLRLAG-----KALLGHVSPRCEYQAGHNKVGSLQYLALALITPK--- 157
Db 112 FDCFSDSAIR-----KALLGHVSPRCEYQAGHNKVGSLQYLALALITPK--- 157
Qy 73 KLXPPRPOSTKSPBELRSKIREMNTKISOESARVNHRLPEGH 116
Db 158 KIRPPLPSVTKLTEDR-----WNKPQKTKHGRGSHTV-NGH 192

RESULT 5
US-08-463-210-10
; Sequence 10, Application US/08463210
; Patent No. 6001977
; GENERAL INFORMATION:
; APPLICANT: CHANG, Nancy T.
; APPLICANT: GALLO, Robert C.
; APPLICANT: WONG-STAAI, Flossie
; TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York

```

;
; COUNTRY: USA
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,210
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/659,339
; FILING DATE: 23-JAN-1985
; REFERENCE/DOCKET NUMBER: 2036-4193US2
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 203 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: HTLV-III
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..203
; OTHER INFORMATION: /note= "sor protein of HTLV-III"
;
; JS-08-463-210-10
;
; Query Match 10.9%; Score 77; DB 3; Length 203;
; Best Local Similarity 27.9%; Pred. No. 0.82;
; Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;
;
; 2y 22 FDMREALRVKSSERLAMLALAG-----MCGHRVLPPTGASAIATVTPKGASM 72
; 123 FDCFSDSAIR-----KALLGHVSPRCEYQAGHNKVGSLQYLALALITPK---- 168
;
; 2y 73 KLKPPRPQSTKSPELRELSRKIREMNKTIQESARVNHRLPEGH 116
; 169 KIKPLPSPVTKLTEDR-----WNKPKQTKYGRGSHTM-NGH 203
;
; RESULT 6
; JS-08-824-878-1
; Sequence 1, Application US/08824878
; Patent No. 5981221
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HISTONE FUSION PROT
; MEDIUM TYPE: Diskette
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/353,688
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/824,878
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
;
;
;
;
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/824,878
; FILING DATE: Filled Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0255 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4186
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 373 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRSTNOT05
; CLONE: 2297753
;
; US-08-824-878-1
;
; Query Match 10.8%; Score 76.5; DB 2; Length 373;
; Best Local Similarity 23.3%; Pred. No. 2.2;
; Matches 31; Conservative 20; Mismatches 61; Indels 21; Gaps 3;
;
; QY 26 REALRVKSSERLAMLALAGMCGHRVLPPTGASAIATVTPKGASMKLK----PPRPQS 81
; DB 79 RHLLAVANDELNQLLKGVITIASGGVLPNIHPPELLA---KTRGSKGLEAITTPPAKK 135
;
; QY 82 TKSP-----LRELSRKIREMNKTIQESARVNHRLPEGHPLLEKRAEYFR 127
; DB 136 AKSPSQKPKVSKKAGGKKGARKSKKQGEVSKAASDNNRGEHLPGDFTVLSTKSLFLG 195
;
; QY 128 HLRSLSQGVNRL 140
; DB 196 QKLNLIHSEISNL 208
;
; RESULT 7
; US-09-353-688-1
; Sequence 1, Application US/09353688
; Patent No. 6136314
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HISTONE FUSION PROT
; MEDIUM TYPE: Diskette
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/353,688
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/824,878
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
;
;
;
;

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; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/824,878
;   FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PP-0255 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-845-4186
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 373 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: BRSTNOT05
;   CLONE: 2297753
; JS-08-824-878-1
; Query Match      10.8%; Score 76.5; DB 2; Length 373;
; Best Local Similarity 23.3%; Pred. No. 2.2;
; Matches 31; Conservative 20; Mismatches 61; Indels 21; Gaps 3;
; QY 26 REALRVKSSERLAMLALACMGCHRYLPGTGASAIATVTPKGASKLK-----PPRPQS 81
; DB 79 RHLLAVANDSELNQLLGVTIAGSGVLPIHPELLA---KRGSKGLEAITPTPPAKX 135
; QY 82 TKSP-----LRLESRKIREMKNKTISOESARVNHLPEGHPLLEKRAEYFR 127
; DB 136 AKSPQKKPVSKGAGKGGARKKKQGEVSKAASDNNRGEHLPGFTVLSTKSFLG 195
; QY 128 HLRSLKSQGVNRL 140
; DB 196 OKNLNIHSEISNL 208
; RESULT 7
; US-09-353-688-1
; Sequence 1, Application US/09353688
; Patent No. 6136314
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HISTONE FUSION PROT
; TITLE OF INVENTION: EIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/353,688
;   FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/824,878
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.

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; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/824,878
;   FILING DATE: Filed Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.
;   REGISTRATION NUMBER: 36,749
;   REFERENCE/DOCKET NUMBER: PP-0255 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 415-855-0555
;   TELEFAX: 415-845-4186
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 373 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: BRSTNOT05
;   CLONE: 2297753
; JS-08-824-878-1
; Query Match      10.8%; Score 76.5; DB 2; Length 373;
; Best Local Similarity 23.3%; Pred. No. 2.2;
; Matches 31; Conservative 20; Mismatches 61; Indels 21; Gaps 3;
; QY 26 REALRVKSSERLAMLALACMGCHRYLPGTGASAIATVTPKGASKLK-----PPRPQS 81
; DB 79 RHLLAVANDSELNQLLGVTIAGSGVLPIHPELLA---KRGSKGLEAITPTPPAKX 135
; QY 82 TKSP-----LRLESRKIREMNKTISOESARVNHLPEGHPLLEKRAEYFR 127
; DB 136 AKSPQKKPVSKGAGKGGARKKKQGEVSKAASDNNRGEHLPGFTVLSTKSFLG 195
; QY 128 HLRSLKSQGVNRL 140
; DB 196 OKNLNIHSEISNL 208
; RESULT 7
; US-09-353-688-1
; Sequence 1, Application US/09353688
; Patent No. 6136314
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HISTONE FUSION PROT
; TITLE OF INVENTION: EIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/353,688
;   FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/824,878
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME: Billings, Lucy J.

```

RESULT 11
US-09-252-991A-27087
; Sequence 27087, Application US/09252991A
; Patent No. 6551795

RESULT 9
US-09-252-991A-3033
; Sequence 3033; Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:

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; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27087
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27087

Query Match 10.5%; Score 74; DB 4; Length 383;
Best Local Similarity 29.4%; Pred. No. 4.3;
Matches 32; Conservative 9; Mismatches 42; Indels 26; Gaps 5;

QY 30 LRVKSSERLMLR-----ALAGWCHRVLPCTGASAIATVTPKGSMK-----LKPP 77
Db 139 LRAAQRRIPLRRRLRGAGGAGGAGGALFAGAEVGVHVPQGHGAADRELFGLQPP 198
QY 78 ----RPOSTKSPFLRSKIRENMKNTISQESAR-----VNHRLPEG 115
Db 199 ARTRPGAQGGRLRLR---PAPRTAGSELASRPVYPHLLNQLRLPAG 244

RESULT 12
US-09-252-991A-32808
; Sequence 32808, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 32808
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32808

Query Match 10.2%; Score 72.5; DB 4; Length 248;
Best Local Similarity 29.6%; Pred. No. 3.4;
Matches 32; Conservative 10; Mismatches 41; Indels 25; Gaps 6;

QY 33 KSSERLMLRALAGWCHRVLPCTGASAIATVTPKGSMKLPKPPRQST-----KSP 87
Db 80 RSNLSLCLRRSRCC-----ARFCSCTACPR--ARPPRPRAPTSDSPAKPPI 128
QY 88 RLSKIRENMKNTISQESARVNHRLPEGHPLLEKRAE-----YFRHLR 130
Db 129 RPTSMKIHCMNRILDQEVPRSTDCP-GHP---ARAEPAPGVYSPHSR 172

RESULT 13
US-08-911-853-2
; Sequence 2, Application US/08911853
; Patent No. 6048710
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijbert
; APPLICANT: Quax, Wilhelms J.

```

```

; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/911,853
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/699,092
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: GC361-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-846-7620
; TELEFAX: 650-845-6504
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 342 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-911-853-2

Query Match 10.2%; Score 72.5; DB 3; Length 342;
Best Local Similarity 28.2%; Pred. No. 5.3;
Matches 29; Conservative 16; Mismatches 39; Indels 19; Gaps 4;

QY 24 VMREALLRVKSSERLMLRALAGWCHRVLPCTGASAIATVTPKGSMKLPKPPRQST 82
Db 101 VLEDQLVH---SERLSIGRLAAGVAHGNVTGTACLAQNL-----REERE 145
QY 83 KSPFLRSKIRENMKNTISQESARVNHRLPEGHPLLEKRAEY 125
Db 146 GDEELGEISNQILDQTKRISR---IVQSLMNFHAGAQOQRAEY 185

RESULT 14
US-09-479-409-2
; Sequence 2, Application US/09479409
; Patent No. 6225106
; GENERAL INFORMATION:
; APPLICANT: Gerritse, Gijbert
; APPLICANT: Quax, Wilhelms J.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
; TITLE OF INVENTION: EXPRESSION LEVELS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genencor International
; STREET: 925 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1013
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/479,409

```

```

US-09-479-453-2
Query Match      10.2%; Score 72.5; DB 4; Length 342;
Best Local Similarity 28.2%; Pred.No.5.3;
Matches 29; Conservative 16; Mismatches 39; Indels 19; Gaps 4;

QY   24 VMREALLRVKSSERLAMLALACMGCHRV-LPGTGASAIATVTPKGSMKLKPPRPOST 82
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   101 VLEDQLVH---SERLASIGLAAGVAHEIGNPVTGIACLAQN-----REERE 145

QY   83 KSPBELSKIREMKNKTISQSARVNHLPEGHPLLEKRAEY 125
     ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db   146 GDEELGEISNQILDOTKRISR---IVQSLMNFHAHQOORAEY 185
     ||| : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 16
US-09-252-991A-26169
; Sequence 26169, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: 107196.136
; CURRENT FILING DATE: 1999-02-18 / 252,991A
; PRIOR FILING DATE: 1998-02-18 / 788
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26169
; LENGTH: 282
; TYPE: PRG
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-26169

Query Match      10.1%; Score 71.5; DB 4; Length 282;
Best Local Similarity 28.8%; Pred.No.5.3;
Matches 42; Conservative 10; Mismatches 63; Indels 31; Gaps 7;

QY   14 NRPTFGTDFVREALLRVKSSERLAMLR-----ALAGMCGRHVLPST---GASAIATV 65
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   138 SRPAPGG-----RSRTIRASAPHRSARPWTGTTRKAGSGGGLRGADRCGCAGSAT- 191
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY   66 TPKGASMKLKPPR-----PQSTKSPELRELRSKIREMKNTISQESARVNHLRP 113
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   192 TPAPRSVPSPSPARYPAVAGRDRSRPPAPGPSASRLSRTDPRGNRAPSPAGNREIH--P 249
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY   114 EGHPL---LEKRAEYFRHLRLSKSQ 136
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   250 AQCPFLRHARQAOWLDGKRTRXNG 275
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 17
US-08-894-997-50
; Sequence 50, Application US/08894997A
; Patent No. 627690
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J
; TITLE OF INVENTION: NEURON-RESTRICTIVE SILENCER FACTOR
; FILE REFERENCE: 17810-502 NRSF
; CURRENT APPLICATION NUMBER: US/08/894,997A
; CURRENT FILING DATE: 1998-01-06
; EARLIER APPLICATION NUMBER: PCT/US96/02817
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: 08/398,590
; EARLIER FILING DATE: 1995-03-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 50
; LENGTH: 976

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US-09-479-453-2
Query Match      10.2%; Score 72.5; DB 4; Length 342;
Best Local Similarity 28.2%; Pred.No.5.3;
Matches 29; Conservative 16; Mismatches 39; Indels 19; Gaps 4;

QY   24 VMREALLRVKSSERLAMLALACMGCHRV-LPGTGASAIATVTPKGSMKLKPPRPOST 82
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   101 VLEDQLVH---SERLASIGLAAGVAHEIGNPVTGIACLAQN-----REERE 145

QY   83 KSPBELRLSKIREMKNKTISQSARVNHLPEGHPLLEKRAEY 125
     ||| : : : : : : : : : : : : : : : : : : : : : : : :
Db   146 GDEELGEISNQILDOTKRISR---IVQSLMNFHAHQOORAEY 185
     ||| : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 16
US-09-252-991A-26169
; Sequence 26169, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: 107196.136
; CURRENT FILING DATE: 1999-02-18 / 252,991A
; PRIOR FILING DATE: 1998-02-18 / 788
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26169
; LENGTH: 282
; TYPE: PRG
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-26169

Query Match      10.1%; Score 71.5; DB 4; Length 282;
Best Local Similarity 28.8%; Pred.No.5.3;
Matches 42; Conservative 10; Mismatches 63; Indels 31; Gaps 7;

QY   14 NRPTFGTDFVREALLRVKSSERLAMLR-----ALAGMCGRHVLPST---GASAIATV 65
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   138 SRPAPGG-----RSRTIRASAPHRSARPWTGTTRKAGSGGGLRPDRCGCAGSAT- 191
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY   66 TPKGASMKLKPPR-----PQSTKSPELRELRSKIREMKNKTISQESARVNHLRP 113
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   192 TPAPRSVPSPSPARYPAVAGRDRSRPPAPGPSASRLSRTDRFNGRAPSPAGNREIH--P 249
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY   114 EGHPL---LEKRAEYFRHLRLSKSQ 136
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   250 AQCPFLRHARQAOWLDGKRTRXHG 275
     : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 17
US-08-894-997-50
; Sequence 50, Application US/08894997A
; Patent No. 627690
; GENERAL INFORMATION:
; APPLICANT: Anderson, David J
; TITLE OF INVENTION: NEURON-RESTRICTIVE SILENCER FACTOR
; FILE REFERENCE: 17810-502 NRSF
; CURRENT APPLICATION NUMBER: US/08/894,997A
; CURRENT FILING DATE: 1998-01-06
; EARLIER APPLICATION NUMBER: PCT/US96/02817
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: 08/398,590
; EARLIER FILING DATE: 1995-03-03
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 50
; LENGTH: 976

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(976)
; OTHER INFORMATION: Human NSRF
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(976)
; OTHER INFORMATION: Human NSRF
US-08-894-997-50

Query Match          10.1%; Score 71.5; DB 3; Length 976;
Best Local Similarity 27.5%; Pred. No. 29;
Matches 38; Conservative 20; Mismatches 67; Indels 13; Gaps 6;

QY 1 MESTTTTNFVAENRPTTGETFDV---MREALLRVKSSERLAMLRLALAGMCGHRVLPQTG 57
Db 661 IEVAQTAPTQVCEPPVSEPPVRPTKRSSLRKDRAEKLSLLSEMARQ--EQVLMGVG 718
QY 58 ASAAATVTPKGASMKLKEPRQSTKSP--LRELSRKIRENMKTIISOESARVNHRLPEG 115
Db 719 LVFVRDSKLLKGNKAQPPAPPS--PSPKGSREBETPKDQM---VSDGEGTIVFPLKKG 774
QY 116 HPLLEKRAEYFRHLSLK 133
Db 775 GP--EEAGESPAELAAALK 790

RESULT 18
US-09-368-590-2
; Sequence 2, Application US/09368590
; Patent No. 6187563
; GENERAL INFORMATION:
; APPLICANT: Solimena, Michele
; TITLE OF INVENTION: INTERACTING POLYPEPTIDES FOR
; FILE OF INVENTION: AUTOANTIGENS OF AUTOIMMUNE DISEASES
; FILE REFERENCE: 101918-200 (OCR-941)
; CURRENT APPLICATION NUMBER: US/09/368,590
; PRIOR FILING DATE: 1999-08-04
; EARLIER APPLICATION NUMBER: 60/095,657
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2293
; TYPE: PRT
; ORGANISM: Human
US-09-368-590-2

Query Match          10.1%; Score 71.5; DB 3; Length 2293;
Best Local Similarity 24.5%; Pred. No. 95;
Matches 34; Conservative 17; Mismatches 71; Indels 17; Gaps 5;

QY 12 AENRPTTGETFDVMEALLRVKSSERLAMLRLALAGMCGHRVLPQTGASAIATVTPKGAS 71
Db 1899 AEVTRTVG---YVQELKPERLQPRIDELPEIPGVFEPAALPAEPDAETPATP--AA 1952
QY 72 MKLKPPRQSTKSP--LRELSRKIR--ENKNTISOESARVNHRLPE-----GHPLE 120
Db 1953 AEOVPRPERQESADABELPERRRPERQESYDQSEEAARRRRRPERQESAEHAAHSLTL 2012
QY 121 KRAEYFRHLSLKSGVNR 139
Db 2013 GRYEQMERRRRRERLER 2031

RESULT 19
US-09-252-991A-26115
; Sequence 26115, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26115
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26115

Query Match          10.0%; Score 71; DB 4; Length 558;
Best Local Similarity 23.9%; Pred. No. 15;
Matches 22; Conservative 11; Mismatches 31; Indels 28; Gaps 3;

QY 55 GTGASAIATVTPK-----GASKMLKPPRQSTKSPELRELSRKIREMN 98
Db 284 GPAAGAPAGAAQPRLGTAQRHPRRQLREADGRAVRLPADRPEGLPDQP-----RRKVRPRP 339
QY 99 KTISOESARVNH-----LPEGHPLLEKR 122
Db 340 TALGKTADRGHRLQLAVARPLPGGHPAPER 371

RESULT 20
US-09-252-991A-30436
; Sequence 30436, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30436
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30436

Query Match          10.0%; Score 70.5; DB 4; Length 329;
Best Local Similarity 22.6%; Pred. No. 8.5;
Matches 38; Conservative 14; Mismatches 61; Indels 55; Gaps 6;

QY 3 STSTTTNFVAENRPTTGETFDVMEALLRVKSSERL-----AMRLALAGM 47
Db 26 TTSTPTSAATRSASASRPVNPPTCSRSGSERTRALRRFVAGAGRGALRLGL 85
QY 48 C-----GHRVLPQTGASAIATVTPKGASMKLPPRQSTK-----SP 85
Db 86 CQQRPRGRDGRRRPAGRESFGD-----ALRPVVPVAMSRPPRPPCATPGAGAGAP 138
QY 86 ELRELSRKIREMN--KTISOESARVNH-----PEGHPLLEKR 122
Db 139 ADRADGRAALALGHAASIGERGAIVRHLALLRPLGAPPPGPPANQPR 186

RESULT 21
US-09-251-645-12
; Sequence 12, Application US/09251645
; Patent No. 6281413
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
```

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; APPLICANT: Kramer, Vance C.
; APPLICANT: Morgan, Michael K.
; APPLICANT: Anderson, Arne R.
; APPLICANT: Hart, Hope
; APPLICANT: Warren, Gregory W.
; APPLICANT: Dunn, Martha
; APPLICANT: Chen, Jeng S.
; TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
; TITLE OF INVENTION: AND NUCLEIC ACID SEQUENCES CODING THEREFOR
; FILE REFERENCE: CGC1963/A
; CURRENT APPLICATION NUMBER: US/09/251,645
; CURRENT FILING DATE: 1999-02-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
; LENGTH: 954
; TYPE: PRT
; ORGANISM: Photorhabdus luminescens
US-09-251-645-12

Query Match          10.0%; Score 70.5; DB 3; Length 954;
Best Local Similarity 23.0%; Pred. No. 37;
Matches 32; Conservative 22; Mismatches 54; Indels 31; Gaps 5;

QY 3 SYSTTNFVAEN-----RPTGETFVMREALLRVKSSERLAMLRLAGMCGHRVLP 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 694 SPTNATN-VAIRNPVPAKPTLPKASTSSQSTTYPIKAS-----IKPT 737

QY 56 TCASAIATVTPKGASMKLKPPRPOSTKSPRLSKIREMNKTIISOESAR---VNRH 111
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 738 TSGSSITAPLSPVGNKSTPEILSPSTQNSSSAISTNLQKSFILYADNRSPEDMQSK 797

QY 112 LPEGH-----PLEKRAEYF 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 798 FPEGFKAWTFLDTQMARQF 816

RESULT 22
US-09-252-991A-24804
; Sequence 24804, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Bjvick, Lars
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24804
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24804

Query Match          9.9%; Score 70; DB 4; Length 185;
Best Local Similarity 27.8%; Pred. No. 4.4;
Matches 32; Conservative 13; Mismatches 46; Indels 24; Gaps 4;

QY 31 RVKSSERLAMLRLAGMCGHRVLPOTGASAIATVTPKGASMKLKPPRPQSTKSPELREL 90
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 40 RVRS---MAASRAAA-----SAKAGICATASPSHRRPKALPSARRGAVSPASRRL 86

QY 91 -----SRKIREMNKTIQSASRVNHELPEGHPLLEKR---AEYFRHLRLSLKS 134
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 87 LTAPALPSAKARDSSSCSPAASRRKRLPSSSRKLTTRRAALAAFFLPLSALFS 141

RESULT 23
US-09-252-991A-19038
; Sequence 19038, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19038
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19038

Query Match          9.8%; Score 70; DB 4; Length 242;
Best Local Similarity 27.9%; Pred. No. 6.3; 23; Indels 14; Gaps 2;
Matches 19; Conservative 12; Mismatches 23; Indels 14; Gaps 2;

QY 32 VKSSERLAMLRLAGMCGH-----RVLPOTGASAIATVTPKGASMKL-----KPP 77
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 21 IRSCEVAAGKSGKGLCHWSREEDSPCPRIPAVAIAAICATSPRRWTMSLTATARSAG 80

QY 78 RPQSTKSP 85
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 81 APQAASPP 88

RESULT 24
US-08-795-475-6
; Sequence 6, Application US/08795475
; Patent No. 5983390
; GENERAL INFORMATION:
; APPLICANT: Bjvick, Lars
; TITLE OF INVENTION: Sjvbring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,475
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McWaters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 100084.402D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-475-6
```

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/216.894
; FILING DATE: 24-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 85326/102/DRLO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-216-894-4

Query Match          9.8%; Score 69.5; DB 2; Length 354;
Best Local Similarity 22.4%; Pred. No. 12;
Matches 26; Conservative 26; Mismatches 49; Indels 15; Gaps 4;

QY      32 VKSERLAMLRLALAGMCHRVLPVTGSAIAATVTPKGASMKLKPPRQSTKS-BELREL 90
dbb     :|||::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
        193 LKSKYIAW-----PLOGWQTFGGDHPKSLDVLPRGPSQLQAENIITNSKEMTKL 247
QY      91 SRKIRE-----MNKTISQESARVNHLPEGHPLLEKRAEYFFHLSRLXSQGVN 138
dbb     :||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
        248 REKVKAKEKLDAINRKATKLEER-NCAVKAANKAESEAKTQRLITFESENIN 302

RESULT 27
US-09-115-746-4
; Sequence 4, Application US/09115746
; Patent No. 6228601
; GENERAL INFORMATION:
; APPLICANT: Kirchhoff, Louis V.
; APPLICANT: Otsu, Keiko
; TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
; TITLE OF INVENTION: WITH TRYPA NOSOMA CRUZI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115.746
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/216.894
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 85326/102/DELO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 354 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-09-115-746-4

Query Match
Best Local Similarity 9.8%; Score 69.5; DB 3; Length 354;
Matches 26; Conservative 26; Mismatches 49; Indels 15; Gaps 4;

QY 32 VKSSERLAMLALAGMCGHVRVLPQTGASAIATVTPKGASMKLKPPRPOSTKS-PELREL 90
DB 193 LKSSKYIAW-----PLOGWQATFGGDHPKSDLVPRGSPSQLOQAENNITNSKKTML 247

QY 91 SRKIRE-----MNKTIQSASRVNHRPGLPEGHPLLEKRAEYFRHLRLSKSQGVN 138
DB 248 REKVKAKEKLDAINRATKLEER-NOAYKAAKAEBEKAKTFORLITFESIN 302

RESULT 29
US-09-216-894-2
; Sequence 2, Application US/08216894
; Patent No. 5876734
; GENERAL INFORMATION:
; APPLICANT: Kirchoff, Louis V.
; TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 24-MAR-1994
; FILING DATE: 24-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 85326/102/DRLO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 564 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-115-746-2

Query Match
Best Local Similarity 9.8%; Score 69.5; DB 2; Length 564;
Matches 26; Conservative 26; Mismatches 49; Indels 15; Gaps 4;

QY 32 VKSSERLAMLALAGMCGHVRVLPQTGASAIATVTPKGASMKLKPPRPOSTKS-PELREL 90
DB 193 LKSSKYIAW-----PLOGWQATFGGDHPKSDLVPRGSPSQLOQAENNITNSKKTML 247

QY 91 SRKIRE-----MNKTIQSASRVNHRPGLPEGHPLLEKRAEYFRHLRLSKSQGVN 138
DB 248 REKVKAKEKLDAINRATKLEER-NOAYKAAKAEBEKAKTFORLITFESIN 302

RESULT 29
US-09-115-746-2
; Sequence 2, Application US/09115746
; Patent No. 6228601

```

```

; GENERAL INFORMATION:
; APPLICANT: Kirchoff, Louis V.
; APPLICANT: Otsu, Keiko
; TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/216,894
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 85326/102/DRLO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 564 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-115-746-2

Query Match
Best Local Similarity 9.8%; Score 69.5; DB 3; Length 564;
Matches 26; Conservative 26; Mismatches 49; Indels 15; Gaps 4;

QY 32 VKSSERLAMLALAGMCGHVRVLPQTGASAIATVTPKGASMKLKPPRPOSTKS-PELREL 90
DB 193 LKSSKYIAW-----PLOGWQATFGGDHPKSDLVPRGSPSQLOQAENNITNSKKTML 247

QY 91 SRKIRE-----MNKTIQSASRVNHRPGLPEGHPLLEKRAEYFRHLRLSKSQGVN 138
DB 248 REKVKAKEKLDAINRATKLEER-NOAYKAAKAEBEKAKTFORLITFESIN 302

RESULT 30
US-08-216-894-8
; Sequence 8, Application US/08216894
; Patent No. 5876734
; GENERAL INFORMATION:
; APPLICANT: Kirchoff, Louis V.
; APPLICANT: Otsu, Keiko
; TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25

```

```
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/216,894
/ FILING DATE: 24-MAR-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BENT, Stephen A.
/ REGISTRATION NUMBER: 29,768
/ REFERENCE/DOCKET NUMBER: 85326/102/DRLO
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 643 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/
US-08-216-894-8

Query Match      9.8%; Score 69.5; DB 2; Length 643;
Best Local Similarity 22.4%; Pred. No. 28;
Matches 26; Conservative 26; Mismatches 49; Indels 15; Gaps 4;

QY 32 VKSSERLAMLALAGMCGHVRVLPFGTGASAIATVTPKGASMKLKPFPQSTKS-PELREL 90
Db 193 LKSSKYIAW-----PLQGWAATFGGDHPKSDLVPRGSPSQLOQAENNITNSKKENTKL 247

QY 91 SRKIRE-----MNKTIQESARVNNHRLPEGHPLLEKRAEYFRHLRLSKSQGVN 138
Db 248 REKVKAKEKLDAINRATKLEBER-NQAYKAAHKAEBEAKTFORLITFESENIN 302

RESULT 31
US-09-115-746-8
; Sequence 8, Application US/09115746
; Patent No. 6228601
; GENERAL INFORMATION:
; APPLICANT: Kirchhoff, Louis V.
; TITLE OF INVENTION: POLYPEPTIDES FOR DIAGNOSING INFECTION
; TITLE OF INVENTION: WITH TRYPAOSOMA CRUZI
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,746
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/216,894
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 85326/102/DRLO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 643 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-09-115-746-8
Query Match      9.8%; Score 69.5; DB 3; Length 643;
Best Local Similarity 22.4%; Pred. No. 28;
Matches 26; Conservative 26; Mismatches 49; Indels 15; Gaps 4;

QY 32 VKSSERLAMLALAGMCGHVRVLPFGTGASAIATVTPKGASMKLKPFPQSTKS-PELREL 90
Db 193 LKSSKYIAW-----PLQGWAATFGGDHPKSDLVPRGSPSQLOQAENNITNSKKENTKL 247

QY 91 SRKIRE-----MNKTIQESARVNNHRLPEGHPLLEKRAEYFRHLRLSKSQGVN 138
Db 248 REKVKAKEKLDAINRATKLEBER-NQAYKAAHKAEBEAKTFORLITFESENIN 302

RESULT 32
US-09-252-991A-19375
; Sequence 19375, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19375
; LENGTH: 671
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
/
US-09-252-991A-19375

Query Match      9.8%; Score 69.5; DB 4; Length 671;
Best Local Similarity 28.5%; Pred. No. 29;
Matches 41; Conservative 12; Mismatches 56; Indels 35; Gaps 8;

QY 15 RPTFGETFDYMR---ALLRVKSSERLAMLRLAGMCGHVRVLPFGTGASAIATVTPKGAS 71
Db 455 RP--GETGRVARHPGGAHFR-----RIPRCRPGAPRLGLQFGTGTGTGGAADQE--- 504

QY 72 MKLPPRPQSTKSPLELSR-----KIREMNKTIQESA-----RVNH----- 110
Db 505 RRLRPRPREVR-FRLFRLPRAGGDFRALAVPRLRQRPNDVLHQRHAAPRRQGHLLRM 563

QY 111 RLPEGHPLLEKRAEYFRHLRLSKS 134
Db 564 RFPAGLPALPQRLHRRSRVPRS 587

RESULT 33
US-09-252-991A-30831
; Sequence 30831, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30831
; LENGTH: 232
; TYPE: PRT
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; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-30831

Query Match 9.7%; Score 69; DB 4; Length 232;
 Best Local Similarity 25.6%; Pred. No. 7.7;
 Matches .22; Conservative 14; Mismatches 34; Indels 16; Gaps 4;

QY 49 GHRVPGTGSAAIAATVTPKASMKLKPQSTKSPEL-----RELRSKIREMNKTIS 102
 DB 121 GHRV--AGGSATATAP-----ARPRGSRVAFGIPARSFARVHRRLATLHRQPO 172
 QY 103 QSARVNHLPEGHPLLEKRAEYFRH 128
 DB 173 PQLRTANGKIP--RPKQTNRSNENFLH 196

RESULT 34
 US-09-252-991A-25526
 ; Sequence 25526 Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25526
 ; LENGTH: 411
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25526

Query Match 9.7%; Score 69; DB 4; Length 411;
 Best Local Similarity 30.5%; Pred. No. 17;
 Matches 32; Conservative 12; Mismatches 53; Indels 8; Gaps 5;

QY 14 NRPTGCTGVNREALLRVKSSERLAMLRLALAGMCGHRVLPFGTGASAI--AATVTPKAS 71
 DB 128 HRPLQSGRLRQLLR--RAPAHLGQRAGNAGR--TTGGAGADRRLRHRQFAP 184
 QY 72 MKLKPQSTKSPELRELSRKIREMNKTISQESARVNHLPEGH 116
 DB 185 RSGRRPRGSPHAGRLRRRRHARRH--RQHPPRPAHRQF--GH 226

RESULT 35
 US-09-252-991A-24836
 ; Sequence 24836 Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 24836
 ; LENGTH: 454
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24836

Query Match 9.7%; Score 69; DB 4; Length 454;
 Best Local Similarity 28.1%; Pred. No. 19;
 Matches 27; Conservative 13; Mismatches 48; Indels 8; Gaps 3;

QY 26 REALLRVKSSERLAMLRLALAGMCGHRVLPFGTGASAIATVTPKASMKLKPQSTK 83
 DB 110 RHQLWRLPGGQPQVARGALAGLAGDLPRLGLADAQAARPRGSORIPQPDGRQOP 169
 QY 83 KSPLELSRKIREMNKTISQESARVNH-----RLP 113
 DB 170 SPAGLRGIPRCAAGGVVQLCAALDHHFFRRLP 205

RESULT 36
 US-09-252-991A-32102
 ; Sequence 32102 Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 32102
 ; LENGTH: 461
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-32102

Query Match 9.7%; Score 69; DB 4; Length 451;
 Best Local Similarity 26.8%; Pred. No. 20;
 Matches 30; Conservative 15; Mismatches 57; Indels 10; Gaps 3;

QY 25 MREALLRVKSSERLAMLRLALA-GMCGHRVLPFGTGASAIATVTPKASMKLKPQSTK 83
 DB 309 LRQPAQVAYGQALAEQFVLALGTAGHRAAPAQAQHA-----KGAAGHLHPRHVERQ 361
 QY 84 SPLELSRKIREMNKTISQESARVNHLPEGHPLLEKRAEYFRHLRLSKSO 135
 DB 362 GMEVEEPFAD--EIADTIQGVRAEHGDFLGAADQVHLRFRPLQVERPQ 411

RESULT 37
 US-09-413-814-3
 ; Sequence 3 Application US/09413814
 ; Patent No. 6225064
 ; GENERAL INFORMATION:
 ; APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
 ; APPLICANT: Bristol-Myers Squibb, Co.
 ; APPLICANT: Beyer, Stefan
 ; APPLICANT: Bloecker, Helmut
 ; APPLICANT: Brandt, Petra
 ; APPLICANT: Cino, Paul M
 ; APPLICANT: Dougherty, Brian A
 ; APPLICANT: Goldberg, Steven L
 ; APPLICANT: Hoffe, Gerhard
 ; APPLICANT: Mueller, Joachim
 ; APPLICANT: Reichenbach, Hans
 ; TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
 ; TITLE OF INVENTION: heteropolyketide compounds
 ; FILE REFERENCE: PCT/US 99/23535
 ; CURRENT APPLICATION NUMBER: US/09/413,814
 ; CURRENT FILING DATE: 1999-10-07
 ; EARLIER APPLICATION NUMBER: DE 198 46 493.2
 ; EARLIER FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: PatentIn Ver. 2.1

; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-30831

Query Match 9.7%; Score 69; DB 4; Length 232;
 Best Local Similarity 25.6%; Pred. No. 7.7;
 Matches .22; Conservative 14; Mismatches 34; Indels 16; Gaps 4;

QY 49 GHRVLPGTGASAIATVTPKASMKLKPDPQSTKSPEL-----RELRSKIREMNKTIS 102
 DB 121 GHRVLP--AGGSATATAP-----ARPRGSRVAFGIPARSFARVHRRLATLHRQPO 172
 QY 103 QSARVNHLPEGHLPLEKRAEYFRH 128
 DB 173 PQLRTANGKIP--RPKQTNRSNFHL 196

RESULT 34
 US-09-252-991A-25526
 ; Sequence 25526 Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 25526
 ; LENGTH: 411
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25526

Query Match 9.7%; Score 69; DB 4; Length 411;
 Best Local Similarity 30.5%; Pred. No. 17;
 Matches 32; Conservative 12; Mismatches 53; Indels 8; Gaps 5;

QY 14 NRPTGCTGVNREALLRVKSSERLAMLRLALAGMCGHRVLPFGTGASAI--AATVTPKAS 71
 DB 128 HRPLQSGRLRQLLR--RAPHLGQRAGNAGR--TTGGAGADRRLRHRQFAP 184
 QY 72 MKLKPDPQSTKSPELRELSRKIREMNKTISQESARVNHLPEGH 116
 DB 185 RSGRRPRGSPHAGRLRRRRHARRH--RQHPPRPAHRQF-GH 226

RESULT 35
 US-09-252-991A-24836
 ; Sequence 24836 Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 24836
 ; LENGTH: 454
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24836

Query Match 9.7%; Score 69; DB 4; Length 454;
 Best Local Similarity 28.1%; Pred. No. 19;
 Matches 27; Conservative 13; Mismatches 48; Indels 8; Gaps 3;

QY 26 REALLRVKSSERLAMLRLALAGMCGHRVLPFGTGASAIATVTPKASMKLKPDPQSTK 83
 DB 110 RHQLWLPFGDPQPVARGALAGLAGDLPRLGLADAQAARPRGSRIPQDPDGRQOP 169
 QY 83 KSPELRELSRKIREMNKTISQESARVNH-----RLP 113
 DB 170 SPAGLRGIPRCAAGGVVQLCAALDHHFFRRLP 205

RESULT 36
 US-09-252-991A-32102
 ; Sequence 32102 Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 32102
 ; LENGTH: 461
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-32102

Query Match 9.7%; Score 69; DB 4; Length 451;
 Best Local Similarity 26.8%; Pred. No. 20;
 Matches 30; Conservative 15; Mismatches 57; Indels 10; Gaps 3;

QY 25 MREALLRVKSSERLAMLRLALA-GMCGHRVLPFGTGASAIATVTPKASMKLKPDPQSTK 83
 DB 309 LRQPAQVAYGQALAEQFVLALGAGHRAAPAQAQHA-----KGAAGHLPHRVERQ 361
 QY 84 SPLEBELSEKIREMNKTISQESARVNHLPEGHLPLEKRAEYFRHLRLSKSO 135
 DB 362 GMEVEEPFAD--EIADTIQGVRAEHGDFLGAADQVHLRFRPLQVERPQ 411

RESULT 37
 US-09-413-814-3
 ; Sequence 3 Application US/09413814
 ; Patent No. 6225064
 ; GENERAL INFORMATION:
 ; APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
 ; APPLICANT: Bristol-Myers Squibb, Co.
 ; APPLICANT: Beyer, Stefan
 ; APPLICANT: Bloecker, Helmut
 ; APPLICANT: Brandt, Petra
 ; APPLICANT: Cino, Paul M
 ; APPLICANT: Dougherty, Brian A
 ; APPLICANT: Goldberg, Steven L
 ; APPLICANT: Hoffe, Gerhard
 ; APPLICANT: Mueller, Joachim
 ; APPLICANT: Reichenbach, Hans
 ; TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
 ; TITLE OF INVENTION: heteropolyketide compounds
 ; FILE REFERENCE: PCT/US 99/23535
 ; CURRENT APPLICATION NUMBER: US/09/413,814
 ; CURRENT FILING DATE: 1999-10-07
 ; EARLIER APPLICATION NUMBER: DE 198 46 493.2
 ; EARLIER FILING DATE: 1998-10-09
 ; NUMBER OF SEQ ID NOS: 107
 ; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 3
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-413-814-3

Query Match 9.7%; Score 69; DB 3; Length 553;
Best Local Similarity 24.3%; Pred. No. 26;
Matches 34; Conservative 15; Mismatches 61; Indels 30; Gaps 4;

QY 11 VAENRPTFGTFDYMREALLRVKSSERLAMLRLALAGMCGHRVLPGTGASAIATVTPKGA 70
Db 259 VLEPPRLGELRDGIPRPL-----ERL-VARMLAKNAGERPRDGAATAAELAAVAGEGL 311

QY 71 SMKLPKPPRQSTKSPRLSRKI-----RENNKTIISQESARVNRHLPFGCHPLLE 120
Db 312 SIGASVAAPAAPGSAITTAERKVMCVILADGGAEAGATLSEDDGAA----- 359

QY 121 KRAEYFRHLRLSKSQGVNRL 140
Db 360 -RAEALRDIAARHGRLDRL 378

RESULT 38
US-07-977-434-8
; Sequence 8, Application US/07977434
; Patent No. 5466591
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7
; SOFTWARE: Wordperfect 2.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07977.434
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,490
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,466
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 590,213
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,394
; FILING DATE: 15-MAY-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 143,441
; FILING DATE: 12-JAN-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 063,509
; FILING DATE: 17-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,241
; FILING DATE: 22-AUG-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 746,121
; FILING DATE: 15-AUG-1991
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US90/07641
; FILING DATE: 21-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 585,471
; FILING DATE: 20-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 455,611
; FILING DATE: 22-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 609,157
; FILING DATE: 02-NOV-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 557,517
; FILING DATE: 24-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Luann Cserr
; REGISTRATION NUMBER: 31,822
; REFERENCE/DOCKET NUMBER: Case No. 5466591 8753
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2972
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 834 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-977-434-8

Query Match 9.7%; Score 69; DB 1; Length 834;
Best Local Similarity 23.7%; Pred. No. 45;
Matches 44; Conservative 27; Mismatches 53; Indels 62; Gaps 10;

QY 1 MESTSTTTNFVAENRPTFGT-TFDVMREALL-----RVKSSERLAML-----RAL 44
Db 382 LDPSNTTPEGVA--RRYGGEWTEDAHRALLAERLQONLLERLKGEKJLWLYOEVEKPL 439

QY 45 AGMCGHRVLPGTGASAIATVTPKGSMLKPKPPRPOSTKSPRLSRKI----- 94
Db 440 SRVLAH--MEATGVRLDVAYL--KALSLEL-----AEEIRLEEVEVFLAGHPFNL 486

QY 95 ---RENNKTIISQ-----SARVNRHLPFGCHPLLEKRAEYFRHLRLSKS 134
Db 487 NSRDQLERVLFDLRLPALGKTQKTRSTSAVLEALREAHPIVEKILQH-RELTKLKN 545

QY 135 QGVNRL 140
Db 546 TVVDPL 551

RESULT 39
US-08-458-819-8
; Sequence 8, Application US/08458819
; Patent No. 5795762
; GENERAL INFORMATION:
; APPLICANT: Gelfand, David H.
; APPLICANT: Abramson, Richard D.
; TITLE OF INVENTION: 5' TO 3' EXONUCLEASE MUTATIONS OF
; TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; ZIP: 07110-1199
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: 7
; SOFTWARE: Wordperfect 2.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08458,819
; FILING DATE: 02-JUN-1995

Query Match	9.7%	Score 69;	DB 1;	Length 834;
Best Local Similarity	23.7%	Pred. No. 45;		
Matches	44;	Conservative 27;	Mismatches 53;	Indels 62; Gaps 10;
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QY	45	AGMCGRVLPQTGASAJAATVTPKGASMKLKPPOSTKPELRLEISRKI-----	94	
Db	440	SRVLAH--MEATGVRLDVAVL--KAISLEL-----AEBIRLEEEVFRLAGHPNPL	486	
QY	95	---REMKNXTISQE-----SARVNHRLPEGHFPLEKKAEEVFRHLRSUKS	134	
Db	487	NSRQGLELVFDELRLPALGKTQTKGRKSTSAAVLEALREAHPIVEKILQH--REITKLEN	545	
QY	135	QGVNRL	140	

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; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 834 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-07035-8

Query Match          9.7%; Score 69; DB 5; Length 834;
Best Local Similarity 23.7%; Pred. No. 45;
Matches 44; Conservative 27; Mismatches 53; Indels 62; Gaps 10;

QY 1 MESTSTTTNFVAENRPTFGE-TFDVMREALL-----RVKSSRLAML-----RAL 44
Db 382 LDPSNTTPEGVA--RRYGEWTEDAAHALLAERLQONLLERLKGEEKLLWLYQVEKPL 439
QY 45 AGMCGHRLVPTGASAIATVTPKGASMKLPPRPQSTKSPELRELSRKI----- 94
Db 440 SRVLAH--MEATGVRLDVAYL--KALSLEL-----AEEIRLEEVEVFRLAGHPFNL 486
QY 95 ---REMNTTISOE-----SARVNHRLPEGHPLLEKRAEYFRHLRSIKS 134
Db 487 NSRDQLERVLFDLELRLPALGKTQTKGRKSTSAANVLEALREAHPIVEKILQH-RELTCLKN 545
QY 135 QGVNRL 140
Db 546 TYVDPL 551
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Search completed: November 14, 2003, 10:43:08
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 10:41:46 ; Search time 30 Seconds
(without alignments)

858.030 Million cell updates/sec

Title: US-10-087-573-2

Perfect score: 708

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Gapop 10.0 , Gapext 0.5

Searched: 666188 seqs, 182559486 residues

Total number of hits satisfying chosen parameters: 666188

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	638	90.1	285	12	Sequence 2, Appli
3	77	10.9	192	12	Sequence 4, Appli
4	75.5	10.7	839	11	Sequence 180, App
5	75.5	10.7	839	12	Sequence 47, Appl
6	75.5	10.7	839	12	Sequence 202, App
7	73.5	10.4	293	10	Sequence 47, Appl
8	73.5	10.4	293	10	Sequence 231, App
9	73.5	10.4	293	10	Sequence 231, App
10	73.5	10.4	293	10	Sequence 231, App
11	73.5	10.4	293	11	Sequence 231, App
12	73.5	10.4	293	11	Sequence 231, App
13	73.5	10.4	293	11	Sequence 231, App
14	73.5	10.4	293	11	Sequence 231, App
15	73.5	10.4	293	11	Sequence 231, App

16	73.5	10.4	293	11	US-09-978-564A-231	Sequence 231, App
17	73.5	10.4	293	11	US-09-999-833A-231	Sequence 231, App
18	73.5	10.4	293	11	US-09-981-915A-231	Sequence 231, App
19	73.5	10.4	293	11	US-09-978-824-231	Sequence 231, App
20	73.5	10.4	293	11	US-09-918-585A-231	Sequence 231, App
21	73.5	10.4	293	11	US-09-978-423A-231	Sequence 231, App
22	73.5	10.4	293	11	US-09-978-193A-231	Sequence 231, App
23	73.5	10.4	293	11	US-09-999-830A-231	Sequence 231, App
24	73.5	10.4	293	11	US-09-978-757A-231	Sequence 231, App
25	73.5	10.4	293	11	US-09-978-187B-231	Sequence 231, App
26	73.5	10.4	293	11	US-09-978-643A-231	Sequence 231, App
27	73.5	10.4	293	12	US-09-978-375A-231	Sequence 231, App
28	73.5	10.4	293	12	US-09-978-188A-231	Sequence 231, App
29	73.5	10.4	293	12	US-09-978-988A-231	Sequence 231, App
30	73.5	10.4	293	12	US-10-137-870-422	Sequence 422, App
31	73.5	10.4	293	12	US-10-140-018-422	Sequence 422, App
32	73.5	10.4	293	12	US-10-140-021-422	Sequence 422, App
33	73.5	10.4	293	12	US-10-140-274-422	Sequence 422, App
34	73.5	10.4	293	12	US-10-140-471-422	Sequence 422, App
35	73.5	10.4	293	12	US-10-140-807-422	Sequence 422, App
36	73.5	10.4	293	12	US-10-140-922-422	Sequence 422, App
37	73.5	10.4	293	12	US-10-140-924-422	Sequence 422, App
38	73.5	10.4	293	12	US-10-140-926-422	Sequence 422, App
39	73.5	10.4	293	12	US-10-141-698-422	Sequence 422, App
40	73.5	10.4	293	12	US-10-141-702-422	Sequence 422, App
41	73.5	10.4	293	12	US-10-141-704-422	Sequence 422, App
42	73.5	10.4	293	12	US-10-142-421-422	Sequence 422, App
43	73.5	10.4	293	12	US-10-142-432-422	Sequence 422, App
44	73.5	10.4	293	12	US-10-142-767-422	Sequence 422, App
45	73.5	10.4	293	12	US-10-143-031A-231	Sequence 231, App

ALIGNMENTS

RESULT 1

US-10-087-573-2
; Sequence 2, Application US/10087573
; Publication No. US20030165872A1
; GENERAL INFORMATION:
; APPLICANT: SCHETTTERS, Theodorus PM
; APPLICANT: CARCY, Bernard PD
; APPLICANT: DRACULOVSKI, Pascal R
; APPLICANT: CORENFLOT, Andre F
; TITLE OF INVENTION: BABESIA CANIS VACINE
; FILE REFERENCE: SCHETTTERS
; CURRENT APPLICATION NUMBER: US/10/087,573
; CURRENT FILING DATE: 2002-04-28
; PRIOR APPLICATION NUMBER: EP 01200816.5
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Babesia canis
US-10-087-573-2

Query Match	100.0%	Score 708;	DB 12;	Length 141;
Best Local Similarity	100.0%;	Pred. No. 1e-65;		
Matches 141;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MESTSTTNFVAENRPTFGEFDVNR	ALLRKSSERLAMLALAGMCHRVLP	PTGASA 60
DB	1	MESTSTTNFVAENRPTFGEFDVNR	ALLRKSSERLAMLALAGMCHRVLP	PTGASA 60
QY	61	IAATVTPKGASMKLPPRQSTKSP	ELBELSKIREMKNKTSQESARVNH	RLPEGHPLLE 120
DB	61	IAATVTPKGASMKLPPRQSTKSP	ELBELSKIREMKNKTSQESARVNH	RLPEGHPLLE 120
QY	121	KRAEYFRLRLSLKSGQVNRLLI	141	
DB	121	KRAEYFRLRLSLKSGQVNRLLI	141	


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RESULT 2
US-10-087-573-4
; Sequence 4, Application US/10087573
; Publication No. US20030165872A1
; GENERAL INFORMATION:
; APPLICANT: SCHEITERS, Theodorius PM
; APPLICANT: CARCY, Bernard PD
; APPLICANT: DRACULOVSKI, Pascal R
; APPLICANT: GORENLOT, Andre F
; TITLE OF INVENTION: BABESIA CANIS VACCINE
; FILE REFERENCE: SCHEITERS
; CURRENT APPLICATION NUMBER: US/10/087.573
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: EP 01200816.5
; PRIOR FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Babesia canis
US-10-087-573-4

Query Match          90.1%; Score 638; DB 12; Length 285;
Best Local Similarity 94.8%; Pred. No. 4.8e-56;
Matches 128; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MESTSTTNFVAENRPTFGTDFVREALLRVKSSERLALMRLALAGMCHGRVLPGTGASA 60
DB 1 MESTSTTNFVAENRPTFGTDFVREALLRVKSSERLALMRLALAGMCHGRVLPGTGASA 60
QY 61 IAAVTGKASMKLPPRPOSTKSPPELRSKIREMKNKTISOESARVNHRLPEGHPLLE 120
DB 61 IAAVTGKASMKLPPRPOSTKSPPELRSKIREMKNKTISOESARVNHRLPEGHPLLE 120
QY 121 KRAEYFRHLRSLKSQ 135
DB 121 KRAEYFVTLDLRAK 135

RESULT 3
US-10-190-435-180
; Sequence 180, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BAENETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBERG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; FILE REFERENCE: PP18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190.435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 180
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: vif HXB2
US-10-190-435-180

Query Match          10.9%; Score 77; DB 12; Length 192;
Best Local Similarity 27.9%; Pred. No. 4.9;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

QY 22 FDMVREALLRVKSSERLALMRLALAGMCHGRVLPGTGASAIATVTPKGASW 72
DB 22 FDMVREALLRVKSSERLALMRLALAGMCHGRVLPGTGASAIATVTPKGASW 72

RESULT 4
US-09-864-636A-47
; Sequence 47, Application US/09864636A
; Publication No. US20030104378A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allwail, Hatim
; APPLICANT: Bartholomay, Christian
; APPLICANT: Chehak, LuAnne
; TITLE OF INVENTION: Detection of RNA Sequences
; FILE REFERENCE: FORS-04944
; CURRENT APPLICATION NUMBER: US/09/864.636A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 2640
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 47
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-864-636A-47

Query Match          10.7%; Score 75.5; DB 11; Length 839;
Best Local Similarity 28.3%; Pred. No. 51;
Matches 39; Conservative 23; Mismatches 45; Indels 31; Gaps 8;

QY 29 LLRVKSSERLAML-----RALAGMCHGRVLPGTGA-----SAIAATVTPKGASMKLKP 76
DB 418 LXRLEGEERLLWYREVERPISAVLAH--MEATGVRLDVAVLRALSLEVAEEIARLEAEV 475
QY 77 PR-----POSTKSPPELRSR-----KIREMKNKTISOE--SARVNHRLPEGHPLLEKR 122
DB 476 FRLAGHPNLSRD--QLERVLFDELRIPIKXKTKRSTSAVLEALREAHPIVEKI 533
QY 123 AEYFRHLRSLKSQGVNRL 140
DB 534 LQY-RELTKLRSTYIDPL 550

RESULT 5
US-09-758-282-202
; Sequence 202, Application US/09758282
; Publication No. US20030134349A1
; GENERAL INFORMATION:
; APPLICANT: Ma, Wu-Po
; APPLICANT: Lyamichev, Victor I.
; APPLICANT: Kaiser, Michael W.
; APPLICANT: Lyamicheva, Natalie E.
; APPLICANT: Allawi, Hatim T.
; APPLICANT: Schaefer, James J.
; APPLICANT: Neri, Bruce P.
; TITLE OF INVENTION: Improved Enzymes for the Detection of Specific Nucleic
; FILE REFERENCE: FORS-04323
; CURRENT APPLICATION NUMBER: US/09/758.282
; CURRENT FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 280
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 202
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-758-282-202
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Query Match 10.7%; Score 75.5; DB 12; Length 839;
Best Local Similarity 28.3%; Pred. No. 51;
Matches 39; Conservative 23; Mismatches 45; Indels 31; Gaps 8;

QY 29 LLRVKSSRLAML-----PALAGMCHRVLPOTGA-----SAIAATVTPKGASMKLKP 76
DB 418 LKRLGEERLLWLYREVERPLSAVLAH--MEATGVRLDVAVLRALSLEVAEIAELEAEV 475
QY 77 PR-----POSTKSPLELRSR-----KIREMNKTIQSE-SARVNHRLPEGHPLLEKR 122
DB 476 FRLAGHPFNLSRD--QLERVLFDLRIPIKIKTKTKRSTSAAVLEALREAHPIVEKI 533
QY 123 AEFYRHLRSLKSGQVNR 140
DB 534 LQY-RELTKLKSTYIDPL 550

RESULT 6

US-10-084-839-47
; Sequence 47, Application US/10084839
; Publication No. US20030186238A1
; GENERAL INFORMATION:
; APPLICANT: Third Wave Technologies
; APPLICANT: Allawi, Hatim
; APPLICANT: Argue, Brad T.
; APPLICANT: Bartholomay, Christian T.
; APPLICANT: Chehak, LuAnne
; APPLICANT: Curtis, Michelle L.
; APPLICANT: Bis, Peggy S.
; APPLICANT: Hall, Jeff G.
; APPLICANT: Ip, Hon S.
; APPLICANT: Ji, Lin
; APPLICANT: Kaiser, Michael
; APPLICANT: Kwiatkowski, Jr., Robert W.
; APPLICANT: Lukowiak, Andrew A.
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lyamacheva, Natalie E.
; APPLICANT: Ma, Wupo
; APPLICANT: Neri, Bruce P.
; APPLICANT: Olson, Sarah M.
; APPLICANT: Olson-Munoz, Marilyn C.
; APPLICANT: Schaefer, James J.
; APPLICANT: Skrzypczynski, Zbigniew
; APPLICANT: Takova, Tsetska Y.
; APPLICANT: Thompson, Lisa C.
; APPLICANT: Vedvik, Kevin L.
; TITLE OF INVENTION: RNA Detection Assays
; FILE REFERENCE: FORS-06666
; CURRENT APPLICATION NUMBER: US/10/084,839
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 4004
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-084-839-47

Query Match 10.7%; Score 75.5; DB 12; Length 839;
Best Local Similarity 28.3%; Pred. No. 51;
Matches 39; Conservative 23; Mismatches 45; Indels 31; Gaps 8;

QY 29 LLRVKSSRLAML-----PALAGMCHRVLPOTGA-----SAIAATVTPKGASMKLKP 76
DB 418 LKRLGEERLLWLYREVERPLSAVLAH--MEATGVRLDVAVLRALSLEVAEIAELEAEV 475
QY 77 PR-----POSTKSPLELRSR-----KIREMNKTIQSE-SARVNHRLPEGHPLLEKR 122
DB 476 FRLAGHPFNLSRD--QLERVLFDLRIPIKIKTKTKRSTSAAVLEALREAHPIVEKI 533

QY 123 AEFYRHLRSLKSGQVNR 140
DB 534 LQY-RELTKLKSTYIDPL 550
RESULT 7
US-09-978-295A-231
; Sequence 231, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C11
; CURRENT APPLICATION NUMBER: US/09/978,295A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294

RESULT 8

US-09-978-697-231

Sequence 231, Application US/09978697

Patent No. US20020169284A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

Acids Encoding the Same

FILE REFERENCE: P2630P1C27

CURRENT APPLICATION NUMBER: US/09/978,697

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR FILING DATE: 1997-11-03

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/077450

PRIOR FILING DATE: 1998-03-10

PRIOR APPLICATION NUMBER: 60/077632

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077641

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077649

PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/077791

PRIOR FILING DATE: 1998-03-12

PRIOR APPLICATION NUMBER: 60/078004

PRIOR FILING DATE: 1998-03-13

PRIOR APPLICATION NUMBER: 60/078886

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078936

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078910

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/078939

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: 60/079294

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 60/079656

PRIOR FILING DATE: 1998-03-26

PRIOR APPLICATION NUMBER: 60/079664
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079689
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079663
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079728
 PRIOR FILING DATE: 1998-03-27
 PRIOR APPLICATION NUMBER: 60/079786
 PRIOR FILING DATE: 1998-03-27
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 PRIOR FILING DATE: 1998-03-30
 PRIOR APPLICATION NUMBER: 60/079923
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 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080107
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080165
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080194
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 60/080327
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080328
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 PRIOR APPLICATION NUMBER: 60/080333
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080334
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/081070
 PRIOR FILING DATE: 1998-04-08
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 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081195
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081203
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 PRIOR APPLICATION NUMBER: 60/081955
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081817
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 PRIOR APPLICATION NUMBER: 60/081838
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/082568
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 PRIOR APPLICATION NUMBER: 60/082700
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082796
 PRIOR FILING DATE: 1998-04-23
 PRIOR APPLICATION NUMBER: 60/083336
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/083392
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083495

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US-09-978-192A-231
; Sequence 231, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavan, Ivar J.
; APPLICANT: Kuo, Sophia A.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Tran
; TITLE OF INVENTION: Acids Encoding t
; FILE REFERENCE: P2630PLC9
; CURRENT APPLICATION NUMBER: US/09/978
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR APPLICATION NUMBER: 60/079936
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079689

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RESULT 9

; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/079663
 ; PRIOR FILING DATE: 1998-03-27
 ; PRIOR APPLICATION NUMBER: 60/079728
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 ; PRIOR APPLICATION NUMBER: 60/079923
 ; PRIOR FILING DATE: 1998-03-30
 ; PRIOR APPLICATION NUMBER: 60/080105
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/080107
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/080165
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/080194
 ; PRIOR FILING DATE: 1998-03-31
 ; PRIOR APPLICATION NUMBER: 60/080327
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080328
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080333
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/080334
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/081070
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081049
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081071
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081195
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081203
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081229
 ; PRIOR FILING DATE: 1998-04-09
 ; PRIOR APPLICATION NUMBER: 60/081955
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 ; PRIOR APPLICATION NUMBER: 60/081838
 ; PRIOR FILING DATE: 1998-04-15
 ; PRIOR APPLICATION NUMBER: 60/082568
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 ; PRIOR FILING DATE: 1998-04-22
 ; PRIOR APPLICATION NUMBER: 60/082797
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 ; PRIOR APPLICATION NUMBER: 60/082796
 ; PRIOR FILING DATE: 1998-04-23
 ; PRIOR APPLICATION NUMBER: 60/083336
 ; PRIOR FILING DATE: 1998-04-27
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/083392
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 ; PRIOR FILING DATE: 1998-04-29

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 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 10.4%; Score 73.5; DB 10; Length 293;
 Best Local Similarity 28.8%; Pred. No. 20;
 Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

Qy	29	LLRVKSSERLAMLRL---	AGMCGHRVLPQTGASAJAATVTPKGSMKLPKPPQSTKSP	85
Db	69	LLRTNASKQTALGALKKEVGDC	HSCCSGTQAL	107
Qy	86	ELRELSKRREMNKTISQESARVNHLP	GHPLLEKRAEYFHLRLSKSQ	135
Db	108	ELGEAQAKLMEQESALRELRERV	TQGLAEAGRGREDVTELFPALEAVRIQ	158

RESULT 10
 US-09-999-832A-231
 ; Sequence 231, Application US/09999832A
 ; Publication No. US20020192706A1

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kiljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
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; PRIOR APPLICATION NUMBER: 60/085697

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Query Match 10.4%; Score 73.5; DB 10; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSERLAMLAL---AGMCHRVLPDTGASALAAATVTPKGSMKLPKPPPOSTKSP 85
DB 69 LLRTNASKOTAAALGALKEEVGDC-HSCCSGTQAL-----QTTTA- 107
QY 86 ELRELSRKTRKNTKTSQSARVNHRLPE-GHPLLEKRAEYFRLHLSKSQ 135
DB 108 ELGEAQAKLMEQESALRELRERVTOGLAEAGRGREDVRLTFRALEAVRLQ 158

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RESULT 11

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US-09-978-189-231
; Sequence 231, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.

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; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kluavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C7
; CURRENT APPLICATION NUMBER: US/09/978,189
; CURRENT FILING DATE: 2001-10-15
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; PRIOR APPLICATION NUMBER: 60/079663
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; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786

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; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C22
; CURRENT APPLICATION NUMBER: US/09/978,508A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 231
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-978-585A-231

Query Match      10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRVLPOTGASAIATVTPKGASMKLKPPRQSTKSP 85
Db 69 LLRTNASKQTALGALKKEVGDC-HSCCSTQACL-----OTTRA- 107

QY 86 ELRELSRKIREMNKTSQESARVNHRLPE-GHPLLEKRAEYFRHLRLSKSQ 135
Db 108 ELGEAQAKLMEQESALRELRERVTOGLAEGAGRGREDVTELFRALEAVRLQ 158

RESULT 13
US-09-978-585A-231
; Sequence 231, Application US/0978585A
; Publication No. US20030049633A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250

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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C15
; CURRENT APPLICATION NUMBER: US/09/978,585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 231
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-978-585A-231

Query Match      10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRVLPOTGASAIATVTPKGASMKLKPPRQSTKSP 85
Db 69 LLRTNASKQTALGALKKEVGDC-HSCCSTQACL-----OTTRA- 107

QY 86 ELRELSRKIREMNKTSQESARVNHRLPE-GHPLLEKRAEYFRHLRLSKSQ 135
Db 108 ELGEAQAKLMEQESALRELRERVTOGLAEGAGRGREDVTELFRALEAVRLQ 158

RESULT 14
US-09-978-191A-231
; Sequence 231, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978,191A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250

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PRIOR APPLICATION NUMBER:	60/083500
PRIOR FILING DATE:	1998-04-29
PRIOR APPLICATION NUMBER:	60/083742
PRIOR FILING DATE:	1998-04-30
PRIOR APPLICATION NUMBER:	60/084366
PRIOR FILING DATE:	1998-05-05
PRIOR APPLICATION NUMBER:	60/084414
PRIOR FILING DATE:	1998-05-06
PRIOR APPLICATION NUMBER:	60/084441
PRIOR FILING DATE:	1998-05-06
PRIOR APPLICATION NUMBER:	60/084637
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084639
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084640
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084598
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084600
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084627
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/084643
PRIOR FILING DATE:	1998-05-07
PRIOR APPLICATION NUMBER:	60/085339
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085338
PRIOR FILING DATE:	1998-05-13
PRIOR APPLICATION NUMBER:	60/085323

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; PRIOR APPLICATION NUMBER: 60/085580
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LRVKSSERLAMLRL---AGMCHRVLPVGTGASALIAATVTPKGSMLKLPKRPQSTKSP 85
DB 69 LRTNASKQTAALGALKSEVGDG-HSCSGTQQL-----QTTA- 107
QY 86 ELRELSKIREMNKTIISOESARVNHRLPE-GHPLLEKEAEVFRHLRLSKSQ 135
DB 108 ELGEAAQLMEQESALRELRLRVRTQTGLAEAGRGREDVRLTFRALEAVRLQ 158

RESULT 15
US-09-978-403A-231
; Sequence 231, Application US/09978403A
; Publication No. US20030050240A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kiljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Pao, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C17
; CURRENT APPLICATION NUMBER: US/09/978,403A
; CURRENT FILING DATE: 2002-03-19
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
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; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817

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2	PRIOR FILING DATE: 1998-04-15	
3	PRIOR APPLICATION NUMBER: 60/081938	
4	PRIOR FILING DATE: 1998-04-15	
5	PRIOR APPLICATION NUMBER: 60/082568	
6	PRIOR FILING DATE: 1998-04-21	
7	PRIOR APPLICATION NUMBER: 60/082569	
8	PRIOR FILING DATE: 1998-04-21	
9	PRIOR APPLICATION NUMBER: 60/082704	
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11	PRIOR APPLICATION NUMBER: 60/082804	
12	PRIOR FILING DATE: 1998-04-22	
13	PRIOR APPLICATION NUMBER: 60/082700	
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15	PRIOR APPLICATION NUMBER: 60/082797	
16	PRIOR FILING DATE: 1998-04-22	
17	PRIOR APPLICATION NUMBER: 60/082796	
18	PRIOR FILING DATE: 1998-04-23	
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43	PRIOR APPLICATION NUMBER: 60/084366	
44	PRIOR FILING DATE: 1998-05-05	
45	PRIOR APPLICATION NUMBER: 60/084414	
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53	PRIOR APPLICATION NUMBER: 60/084640	
54	PRIOR FILING DATE: 1998-05-07	
55	PRIOR APPLICATION NUMBER: 60/084598	
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63	PRIOR APPLICATION NUMBER: 60/085339	
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65	PRIOR APPLICATION NUMBER: 60/085338	
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67	PRIOR APPLICATION NUMBER: 60/085323	
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69	PRIOR APPLICATION NUMBER: 60/085682	
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71	PRIOR APPLICATION NUMBER: 60/085700	
72	PRIOR FILING DATE: 1998-05-15	
73	PRIOR APPLICATION NUMBER: 60/085689	

Query Match	10.4%;	Score 73.5;	DB 11;	Length 293;
Best Local Similarity	28.8%;	Pred. No. 20;		
Matches 32;	Conservative 13;	Mismatches 41;	Indels 25;	Gaps 5;
QY	29	LLRVKSSERLMLRAL---	AGMCGHRVLPFGTCAISAIAATVTPK	GASKMKLPPRPQSTKSP 85
DB	69	LLRTNASKOTALGALKKEVGDC-HSCCSG	QTQAQL-----	QTTRA- 107
QY	86	ELRLSRKTRKNTKISQESARVHRLPE-GH	PLEKAEYFRHLRSLSQ 135	
DB	108	ELGEAQAKLMEQESALRELRRVTOGLAE	AGRGREDVTELFRALEAVRLQ 158	
RESULT 17				
US-09-999-833A-231				
Sequence 231, Application US/09999833A				
Publication No. US20030054405A1				
GENERAL INFORMATION:				
APPLICANT: Ashkenazi, Avi				
APPLICANT: Baker Kevin P.				
APPLICANT: Botstein, David				
APPLICANT: Desnoyers, Luc				
APPLICANT: Eaton, Dan				
APPLICANT: Ferrara Napoleon				
APPLICANT: Filvaroff, Ellen				
APPLICANT: Fong, Sherman				
APPLICANT: Gao, Wei-Qiang				
APPLICANT: Gerber, Hanspeter				
APPLICANT: Gerritsen, Mary E.				
APPLICANT: Goddard, Audrey				
APPLICANT: Godowski, Paul J.				
APPLICANT: Grimaldi, J. Christopher				
APPLICANT: Gurney, Austin L.				
APPLICANT: Hillan, Kenneth J.				
APPLICANT: Kljavin, Ivar J.				
APPLICANT: Kuo, Sophia S.				
APPLICANT: Napier, Mary A.				
APPLICANT: Pan, James				
APPLICANT: Paoli, Nicholas F.				
APPLICANT: Roy, Margaret Ann				
APPLICANT: Shelton, David L.				
APPLICANT: Stewart, Timothy A.				
APPLICANT: Tumas, Daniel				
APPLICANT: Williams, P. Mickey				
APPLICANT: Wood, William I.				
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic				
TITLE OF INVENTION: Acids Encoding the Same				
FILE REFERENCE: P2630PLC65				
CURRENT APPLICATION NUMBER: US/09/999,833A				
CURRENT FILING DATE: 2001-10-24				
PRIOR APPLICATION NUMBER: 09/918595				
PRIOR FILING DATE: 2001-07-30				
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; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
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; PRIOR APPLICATION NUMBER: 60/082569
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; PRIOR APPLICATION NUMBER: 60/083742
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; PRIOR APPLICATION NUMBER: 60/084366
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; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-07
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; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
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; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
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; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
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; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 10.4%; Score 73.5; DB 11; Length 293;

Best Local Similarity 28.8%; Pred. No. 20;

Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

Qy 29 LLRVKSERLAMLRL---AGMCHRVLPOTGASAIATVTTPKGSMKMLKPPRPQSTKSP 85

Db 69 LLRTNASKQTAAALCALKEEVGDC-HSCCSGTQAL-----QTTA- 107

Qy 86 ELRELSRKIREMNKTIQSASRVNHLPE-GHPLEKRAEYFRLRLSKSQ 135

Db 108 ELGEAQKLMQESALRELRLRVVTQGLAEAGRGREDVRLFRLAEVRLQ 158

RESULT 18

US-09-981-915A-231

; Sequence 231, Application US/09981915A

; Publication No. US20030054986A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Goddard, Audrey E.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: P2630P1C12

; CURRENT APPLICATION NUMBER: US/09/981,915A

; CURRENT FILING DATE: 2001-10-16

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

[illegible]

; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
Query Match 10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;
QY 29 LLRVKSERLMLRAL--AGCMGHRVLPCTGASAIATVTPKGASMKLKPDPPOSTKSP 85
DB 69 LLRTNASKOTAAALGALKEEVGDC-HSCCSGTQAL-----QTTRA- 107
QY 86 ELRELSRKIRENMKTTISQBSARNVRLPE-GHPLEKRAEYFRHLRSLKSQ 135
DB 108 ELGEAQKLMQESALRELRRERVTOGLABAGRGREDVTRTELEAVRLQ 158
RESULT 19
US-09-978-824-231
; Sequence 231, Application US/09978824
; Publication No. US2003005216A1
; GENERAL INFORMATION:
; APPLICANT: Aehkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C14
; CURRENT APPLICATION NUMBER: US/09/978,824
; CURRENT FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
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; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
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; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
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; PRIOR FILING DATE: 1998-03-20
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; PRIOR APPLICATION NUMBER: 60/081838
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; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082569
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704

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; PRIOR APPLICATION NUMBER: 60/085697

Query Match      10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred.No.20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5

QY   29 LLRVKSSRLAMLAL---AGMCGRVLPTGASATAATVTPKGASMKLKPPRPQSTKSP 85
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB   69 LLRTWASQTAAALGALKKEVGDC-HSCCSGTQACL-----QITRA- 107

QY   86 ELRLSUKIRKNKYTKIQESARVNHRLPE-GHPLEKVRARYFRLHLSLKSO 135
    ||| :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
DB   108 ELGEAQAKLMESALRELRRVTQGLAEAGRQREDVRTFLFALEAVRLQ 158


RESULT 20
US-09-918-585A-231
; Sequence 231, Application US/09918585A
; Publication No. US2003060406A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavich, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2430P1C1
; CURRENT APPLICATION NUMBER: US/09/918,585A
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/078004
; PRIOR FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 60/078886
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PRIOR APPLICATION NUMBER: 60/082799	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796	PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796	PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336	PRIOR FILING DATE: 1998-04-27
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PRIOR APPLICATION NUMBER: 60/083495	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545	PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554	PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/083558	PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/083559	PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/083500	PRIOR FILING DATE: 1998-04-30
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PRIOR APPLICATION NUMBER: 60/084366	PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441	PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639	PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640	PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/084643	PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/085339	PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085338	PRIOR FILING DATE: 1998-05-13
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PRIOR APPLICATION NUMBER: 60/085582	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700	PRIOR FILING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/085704	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697	PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086023	PRIOR FILING DATE: 1998-05-15

Query Match
10.4%; Score 73.5; DB 11; Length 293;

Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;
QY 29 LRVKSERLALR-AGMCHRVLPCTGASAIATVTPKGASMKLKPPOSTKSP 85
| | | : : : | | | | | | | | | : : :
Db 69 LLETNASKTAAALGALKEGVGDC-HSCCSGTQAL-----QITRA- 107
QY 86 ELRLSRKIREMNTISQESARVNHRLPE-GHPLLEKRAEYFRHRLSLKSQ 135
| | | : : : | | | : : : | | | : : :
Db 108 ELGEAQAKLMEQESALRELRLRVRTQGLAAGRGREDVRLTFLAEAVRLQ 158

RESULT 21

US-09-978-423A-231
; Sequence 231, Application US/09978423A
; Publication No. US20030069178A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C21
; CURRENT APPLICATION NUMBER: US/09/978,423A
; CURRENT FILING DATE: 2002-05-16
; PRIOR APPLICATION NUMBER: 09/918595
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 10.4%; Score 73.5; DB 11; Length 293;
 Best Local Similarity 28.8%; Pred. No. 20;
 Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLEVKSSERLMLRAL---AGMCGHRVLPQTGASALAAATVTPKGASMKLPPRPQSTKSP 85
 Db 69 LLRTNASKQTAALGALKKEVGDC-HSCCSGTQAL-----QITRA- 107
 QY 86 ELRELSRKIREMNKTTISQESARVNNHLPE-GHPLLEKRAEYFRLRLSLKSQ 135
 Db 108 ELGEAQAKLMEQESALRELREVRVTQGLAEAGRGREDVRLTELFALEAVRLQ 158

RESULT 22

US-09-978-193A-231
 ; Sequence 231, Application US/09978193A
 ; Publication No. US20030073624A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630PLC6
 ; CURRENT APPLICATION NUMBER: US/09/978,193A
 ; CURRENT FILING DATE: 2002-02-21
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
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7	PRIOR APPLICATION NUMBER: 60/083333	
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7	PRIOR APPLICATION NUMBER: 60/085580	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085700	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085689	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085579	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085580	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085700	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085704	
7	PRIOR FILING DATE: 1998-05-15	
7	PRIOR APPLICATION NUMBER: 60/085697	

QY 29 LLRVKSSRLAMLRAL---AGMCGHVLPGTCASAIATAVTPKGASMKLKP RPQSTKSP 85
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Db 69 LURTNASQTAAALCALKEEVGDC-HSCCSGTQAQL-----QTTRA- 101
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Db 108 EIGEQAQKLMEQESALRELRRVVTQGLAEAGRGREDVYRTLFRALEAVRLQ 15

RESULT 24

US-09-978-757A-231

; Sequence 231, Application US/09978757A

; Publication No. US20030083248A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumaas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nu

; FILE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630PIC26

; CURRENT APPLICATION NUMBER: US/09/978,757A

; CURRENT FILING DATE: 2002-03-19

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

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; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

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; PRIOR FILING DATE: 1998-03-20

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; PRIOR APPLICATION NUMBER: 60/079294

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079556

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Query Match      10.4%; Score 73.5; DB 11; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY      29  LLRVKSSRLAMLAL---AGMCQHRVLPCTGASAIATAVTPKGASMKLKPPOSTKSP 85
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Db      59  LLRTNASKQTALGALKEEVGDC-HSCSGTQQL-----OTTRA- 107
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      86  ELRELSRKIRENNWTIGESARVNHLRPE-GHPLLEKRAEYFRLRSKQS 135
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Query Match 10.4%; Score 73.5; DB 11; Length 293;

Best Local Similarity 28.8%; Pred. No. 20;

Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

Qy 29 LLRVKSSERLAMLRLAL---AGMCGHRYLPCTGASAIATAVTTPKGASMKLPPRPQSTKSP 85

Db 69 LLRTNASKQTALCALKEEVGDC-HSCCSTQAL-----QTIRA-107

Qy 86 ELRELSKIREMKNKTSQESARVNNHRLPE-CHPILLEKRAEYFFHLRLSLKSO 135

Db 108 ELGEAQAKLMEQSAURELREVRVTOGLAEAGRGREDVRLTFLEAVRLQ 158

RESULT 25

US-09-978-187B-231
 ; Sequence 231, Application US/09978187B
 ; Publication No. US20030036744A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Deenoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrari, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Geritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavlin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Pacini, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; TITLE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2630P1C5
 ; CURRENT APPLICATION NUMBER: US/09/978.187B
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
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 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/083495
 ; PRIOR FILING DATE: 1998-04-29
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RESULT 26
US-09-978-643A-231
; Sequence 231, Application US/09978643A

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081203
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 10.4%; Score 73.5; DB 12; Length 293;

Best Local Similarity 28.8%; Pred.No.20;

Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

Qy 29 LLVKSSERLMLRAL---AGMCGHVRVLPQTGASATAATVTPKGSMKLPKPPRQSTKSP 85

Db 69 LLRTNASKQTAALGALKKEVGDG-HSCCSTQAL-----QITRA-107

Qy 86 ELRELSKIREMNKTTISQESARVNHRLPE-GHPLLEKRAEYFRLHSLKSQ 135

Db 108 ELGEAQAKLMEQESALRELRLRVTVQGLAEAGRGREDVRLTFLRALEAVRLQ 158

RESULT 29

US-09-978-298A-231

; Sequence 231, Application US/09978298A

; Publication No. US20030134785A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

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; APPLICANT: Kuo, Sophia S.

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; APPLICANT: Pan, James;

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Shelton, David L.

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C2

; CURRENT APPLICATION NUMBER: US/09/978,298A

PRIOR APPLICATION NUMBER: 60/081200	PRIOR FILING DATE: 1998-04-09	PRIOR APPLICATION NUMBER: 60/081229	PRIOR FILING DATE: 1998-04-09	PRIOR APPLICATION NUMBER: 60/081955	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081817	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081819	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081952	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/081838	PRIOR FILING DATE: 1998-04-15	PRIOR APPLICATION NUMBER: 60/082568	PRIOR FILING DATE: 1998-04-21	PRIOR APPLICATION NUMBER: 60/082569	PRIOR FILING DATE: 1998-04-21	PRIOR APPLICATION NUMBER: 60/082704	PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082804	PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082700	PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082797	PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082796	PRIOR FILING DATE: 1998-04-23	PRIOR APPLICATION NUMBER: 60/083336	PRIOR FILING DATE: 1998-04-27	PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-28	PRIOR APPLICATION NUMBER: 60/083392	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083495	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083496	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083499	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083559	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083545	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083554	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083558	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/084441	PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/083500	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083742	PRIOR FILING DATE: 1998-04-30	PRIOR APPLICATION NUMBER: 60/084366	PRIOR FILING DATE: 1998-05-05	PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/084441	PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/084637	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084639	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084640	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084598	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084600	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084627	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/084643	PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/085339	PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      10.4%; Score 73.5; DB 12; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

Qy 29 LLRVKSSERLAMLRAL---AGMCGHRVLPGTGASAIATVTPKGASMKLKPPRPQSTKSP 85
Db 69 LLRTNASKQTAAALGALKKEEVGDC-HSCCSGTQACL-----QTTA- 107

Qy 86 ELRELSRKIRENMKTTISQESARVNHRLPE-GHPLEKRAEYFRHLRLSKSQ 135
Db 108 ELGEAQAKLMEQESALRELRLRVRTQGLAAGRGREDVRLTFRALEAVRLQ 158

RESULT 30
US-10-137-870-422
; Sequence 422, Application US/10137870
; Publication No. US2003013883A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C158
; CURRENT APPLICATION NUMBER: US/10/137,870
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 422
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-870-422

Query Match      10.4%; Score 73.5; DB 12; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

Qy 29 LLRVKSSERLAMLRAL---AGMCGHRVLPGTGASAIATVTPKGASMKLKPPRPQSTKSP 85
Db 69 LLRTNASKQTAAALGALKKEEVGDC-HSCCSGTQACL-----QTTA- 107

Qy 86 ELRELSRKIRENMKTTISQESARVNHRLPE-GHPLEKRAEYFRHLRLSKSQ 135
Db 108 ELGEAQAKLMEQESALRELRLRVRTQGLAAGRGREDVRLTFRALEAVRLQ 158

RESULT 31
US-10-140-018-422
; Sequence 422, Application US/10140018
; Publication No. US20030138885A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C158
; CURRENT APPLICATION NUMBER: US/10/140,018
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 422
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-018-422

Query Match      10.4%; Score 73.5; DB 12; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

Qy 29 LLRVKSSERLAMLRAL---AGMCGHRVLPGTGASAIATVTPKGASMKLKPPRPQSTKSP 85
Db 69 LLRTNASKQTAAALGALKKEEVGDC-HSCCSGTQACL-----QTTA- 107

Qy 86 ELRELSRKIRENMKTTISQESARVNHRLPE-GHPLEKRAEYFRHLRLSKSQ 135
Db 108 ELGEAQAKLMEQESALRELRLRVRTQGLAAGRGREDVRLTFRALEAVRLQ 158

RESULT 32
US-10-140-021-422
; Sequence 422, Application US/10140021
; Publication No. US20030138886A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C155
; CURRENT APPLICATION NUMBER: US/10/137,870
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 422
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-870-422

Query Match      10.4%; Score 73.5; DB 12; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

```


APPLICANT: Smith,Victoria
APPLICANT: Stewart,Timothy A.
APPLICANT: Tumas,Daniel
APPLICANT: Watanabe,Colin K
APPLICANT: Wood,William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C167
CURRENT APPLICATION NUMBER: US/10/140,021
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 422
LENGTH: 293
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-021-422

Query Match 10.4%; Score 73.5; DB 12; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRLVPGTGASAIATVTPKGSMKLPKPPQSTKSP 85
DB 69 LLRTNASKQTALGALKKEVGDC-HSCCSGTQQL-----QTTA- 107

QY 86 ELRLSKIREMKNKTIQESARVNNHRLPE-GHPLLEKRAEYFRHLRLSKSQ 135
DB 108 ELGEAQAKLMEQESALRELRLRVTOGLAEAGRGREDVRTLFRALAEVRLQ 158

RESULT 33
US-10-140-274-422
Sequence 422, Application US/10140274
Publication No. US20030143674A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C167
CURRENT APPLICATION NUMBER: US/10/140,274
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 422
LENGTH: 293
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-274-422

Query Match 10.4%; Score 73.5; DB 12; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRLVPGTGASAIATVTPKGSMKLPKPPQSTKSP 85
DB 69 LLRTNASKQTALGALKKEVGDC-HSCCSGTQQL-----QTTA- 107

QY 86 ELRLSKIREMKNKTIQESARVNNHRLPE-GHPLLEKRAEYFRHLRLSKSQ 135
DB 108 ELGEAQAKLMEQESALRELRLRVTOGLAEAGRGREDVRTLFRALAEVRLQ 158

Db 69 LLRTNASKQTALGALKKEVGDC-HSCCSGTQQL-----QTTA- 107

QY 86 ELRLSKIREMKNKTIQESARVNNHRLPE-GHPLLEKRAEYFRHLRLSKSQ 135
Db 108 ELGEAQAKLMEQESALRELRLRVTOGLAEAGRGREDVRTLFRALAEVRLQ 158

RESULT 34
US-10-140-471-422
Sequence 422, Application US/10140471
Publication No. US20030138887A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C163
CURRENT APPLICATION NUMBER: US/10/140,471
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 422
LENGTH: 293
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-471-422

Query Match 10.4%; Score 73.5; DB 12; Length 293;
Best Local Similarity 28.8%; Pred. No. 20;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRLVPGTGASAIATVTPKGSMKLPKPPQSTKSP 85
Db 69 LLRTNASKQTALGALKKEVGDC-HSCCSGTQQL-----QTTA- 107

QY 86 ELRLSKIREMKNKTIQESARVNNHRLPE-GHPLLEKRAEYFRHLRLSKSQ 135
Db 108 ELGEAQAKLMEQESALRELRLRVTOGLAEAGRGREDVRTLFRALAEVRLQ 158

RESULT 35
US-10-140-807-422
Sequence 422, Application US/10140807
Publication No. US20030134354A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.

```

; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C174
; CURRENT APPLICATION NUMBER: US/10/140,807
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 422
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-807-422

Query Match
Best Local Similarity 10.4%; Score 73.5; DB 12; Length 293;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRVLPCTGASAIATVTPKGASMKLKPPRQSTKSP 85
DB 69 LLRTNASKQTAALGALKKEEVGDC-HSCCSGTQQL-----QTTRA- 107

QY 86 ELRELSRKIREMKNKTISQESARVNHRLPE-GHPLLEKRAEYFRHLRLSKSQ 135
DB 108 ELGEAQAKLMEQSAALRELRERVVTQGLAAGRGREDVRTLFRALAEVRLQ 158

US-10-140-922-422
; Sequence 422, Application US/10140922
; Publication No. US2003013889A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C177
; CURRENT APPLICATION NUMBER: US/10/140,924
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 422
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-924-422

Query Match
Best Local Similarity 10.4%; Score 73.5; DB 12; Length 293;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRVLPCTGASAIATVTPKGASMKLKPPRQSTKSP 85
DB 69 LLRTNASKQTAALGALKKEEVGDC-HSCCSGTQQL-----QTTRA- 107

QY 86 ELRELSRKIREMKNKTISQESARVNHRLPE-GHPLLEKRAEYFRHLRLSKSQ 135
DB 108 ELGEAQAKLMEQSAALRELRERVVTQGLAAGRGREDVRTLFRALAEVRLQ 158

US-10-140-926-422
; Sequence 422, Application US/10140926
; Publication No. US20030134356A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
US-10-140-926-422

Query Match
Best Local Similarity 10.4%; Score 73.5; DB 12; Length 293;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRVLPCTGASAIATVTPKGASMKLKPPRQSTKSP 85
DB 69 LLRTNASKQTAALGALKKEEVGDC-HSCCSGTQQL-----QTTRA- 107

QY 86 ELRELSRKIREMKNKTISQESARVNHRLPE-GHPLLEKRAEYFRHLRLSKSQ 135
DB 108 ELGEAQAKLMEQSAALRELRERVVTQGLAAGRGREDVRTLFRALAEVRLQ 158

US-10-140-922-422
; Sequence 422, Application US/10140922
; Publication No. US2003013889A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C179
; CURRENT APPLICATION NUMBER: US/10/140,922
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 422
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-922-422

Query Match
Best Local Similarity 10.4%; Score 73.5; DB 12; Length 293;
Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRVLPCTGASAIATVTPKGASMKLKPPRQSTKSP 85
DB 69 LLRTNASKQTAALGALKKEEVGDC-HSCCSGTQQL-----QTTRA- 107
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Db 108 ELGEAQAKLMEQESALRELREVRTQGLAAGRGREDVRTLFEALVRLQ 158

RESULT 40

US-10-141-702-422

Sequence 422, Application US/10141702

Publication No. US20030134358A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C208

CURRENT APPLICATION NUMBER: US/10/141,702

CURRENT FILING DATE: 2002-05-08

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 422

LENGTH: 293

TYPE: PRT

ORGANISM: Homo Sapien

US-10-141-702-422

Query Match 10.4%; Score 73.5; DB 12; Length 293;

Best Local Similarity 28.8%; Pred. No. 20;

Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRVLPGTGASAIATVTPKGASMKLKPPRPOSTKSP 85

Db 69 LLRTNASKQTALGALKKEEVGDC-HSCCSGTQACL-----QTTRA- 107

QY 86 ELRELSRKIREMKNKTISQESARVNHRLPE-GHPLLEKRAEYFRHLRLSKSQ 135

Db 108 ELGEAQAKLMEQESALRELREVRTQGLAAGRGREDVRTLFEALVRLQ 158

RESULT 39

US-10-141-698-422

Sequence 422, Application US/10141698

Publication No. US20030134357A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C206

CURRENT APPLICATION NUMBER: US/10/141,698

CURRENT FILING DATE: 2002-05-08

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 422

LENGTH: 293

TYPE: PRT

ORGANISM: Homo Sapien

US-10-141-698-422

Query Match 10.4%; Score 73.5; DB 12; Length 293;

Best Local Similarity 28.8%; Pred. No. 20;

Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRVLPGTGASAIATVTPKGASMKLKPPRPOSTKSP 85

Db 69 LLRTNASKQTALGALKKEEVGDC-HSCCSGTQACL-----QTTRA- 107

QY 86 ELRELSRKIREMKNKTISQESARVNHRLPE-GHPLLEKRAEYFRHLRLSKSQ 135

Db 108 ELGEAQAKLMEQESALRELREVRTQGLAAGRGREDVRTLFEALVRLQ 158

RESULT 40

US-10-141-702-422

Sequence 422, Application US/10141702

Publication No. US20030134358A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.

APPLICANT: Beresini, Maureen

APPLICANT: DeForge, Laura

APPLICANT: Desnoyers, Luc

APPLICANT: Filvaroff, Ellen

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Gurney, Austin L.

APPLICANT: Sherwood, Steven

APPLICANT: Smith, Victoria

APPLICANT: Stewart, Timothy A.

APPLICANT: Tamas, Daniel

APPLICANT: Watanabe, Colin K

APPLICANT: Wood, William

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE REFERENCE: P3330R1C208

CURRENT APPLICATION NUMBER: US/10/141,702

CURRENT FILING DATE: 2002-05-08

Prior Application removed - See Palm or File Wrapper

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 422

LENGTH: 293

TYPE: PRT

ORGANISM: Homo Sapien

US-10-141-702-422

Query Match 10.4%; Score 73.5; DB 12; Length 293;

Best Local Similarity 28.8%; Pred. No. 20;

Matches 32; Conservative 13; Mismatches 41; Indels 25; Gaps 5;

QY 29 LLRVKSSERLAMLRL---AGMCGHRVLPGTGASAIATVTPKGASMKLKPPRPOSTKSP 85

Db 69 LLRTNASKQTALGALKKEEVGDC-HSCCSGTQACL-----QTTRA- 107

QY 86 ELRELSRKIREMKNKTISQESARVNHRLPE-GHPLLEKRAEYFRHLRLSKSQ 135

Db 108 ELGEAQAKLMEQESALRELREVRTQGLAAGRGREDVRTLFEALVRLQ 158

Search completed: November 14, 2003, 10:49:28

Job time : 31 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2003, 10:38:35 ; Search time 43 Seconds
(without alignments)
315.344 Million cell updates/sec

Title: US-10-087-573-2
Perfect score: 708
Sequence: 1 MESSTTTFVAENRPTFGE.....RAEYFRLRLSLKSGVNRLLI 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	12.1	524	A75588	probable protein k
2	84.5	11.9	609	A43906	nuclear phosphopro
3	82	11.6	192	S33981	vif protein - huma
4	82	11.6	239	AG2057	hypothetical prote
5	81.5	11.5	1281	G83405	hypothetical prote
6	81	11.4	192	S42996	viral infectivity
7	80	11.3	464	C83328	hypothetical prote
8	80	11.3	902	T98878	respiratory burst
9	79.5	11.2	3839	T49799	related to TOM1 pr
10	79	11.2	192	S42944	viral infectivity
11	79	11.2	192	S42957	viral infectivity
12	79	11.2	1780	T12722	hypothetical prote
13	78.5	11.1	92	S61809	Malike protein enn
14	78.5	11.1	1120	S90693	mechanosensitive c
15	78.5	11.1	1120	B85544	mechanosensitive c
16	78.5	11.0	1120	H64776	probable membrane
17	78	11.0	171	D96547	hypothetical prote
18	78	11.0	192	S42959	viral infectivity
19	78	11.0	686	F72655	hypothetical prote
20	77.5	10.9	480	A45339	outer capsid prote
21	77	10.9	192	ASLJ83	vif protein - huma
22	77	10.9	192	ASLJNA	vif protein - huma
23	77	10.9	192	S42960	viral infectivity
24	77	10.9	192	S42960	viral infectivity
25	77	10.9	192	S42940	viral infectivity
26	77	10.9	192	S42946	viral infectivity
27	77	10.9	889	H84506	probable retroelem
28	76	10.7	192	S42977	viral infectivity
29	76	10.7	325	E85966	probable aldehyde

30 76 10.7 405 2 E82992 probable FAD-depen
31 76 10.7 408 2 G70522 probable transposa
32 76 10.7 427 2 I49603 transcription regu
33 76 10.7 1021 2 G75403 DNA topoisomerase
34 75.5 10.7 350 2 F97169 sialic acid syntha
35 75 10.6 192 2 S43000 viral infectivity
36 75 10.6 192 2 S42965 viral infectivity
37 75 10.6 606 2 G75302 orocidine 5'-phosp
38 75 10.6 1313 2 A48467 myosin heavy chain
39 75 10.6 1957 2 A45627 myosin heavy chain
40 74.5 10.5 288 2 AE2083 phosphonate metabo
41 74.5 10.5 938 2 T39006 related to yeast z
42 74.5 10.5 1006 2 T42731 atrophin-1 related
43 74 10.5 662 2 D54078 methyl-accepting c
44 74 10.5 908 1 JQ1938 structural core pr
45 73.5 10.4 402 2 S37046 Iga receptor - Str

ALIGNMENTS

RESULT 1

A75588
Probable protein kinase - Deinococcus radiodurans (strain R1)
C/Species: Deinococcus radiodurans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C/Accession: A75588
R/White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.
S.; Smith, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
Science 286, 1571-1577, 1999
A/Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A/Reference number: A75250; MUID:20036896; PMID:10567266
A/Accession: A75588
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-524 <WHI>
A/Cross-references: GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF12449.1; PID:g6460
A/Experimental source: strain R1
C/Genetics:
A/Gene: DRA0332
A/Map position: 2

Query Match 12.1%; Score 86; DB 2; Length 524;

Best Local Similarity 29.0%; Pred. No. 4.5;

Matches 29; Conservative 23; Mismatches 28; Indels 20; Gaps 6;

QY 25 MREALL-----RYKSSERLAMLALAGMCHRVLPCTG-----ASAIAATVTPKASMKLK 75

Db 287 LREAVLSCHMAPRIENRPSA--QAL-----RRILRGEGVTVTAPAAPAPQPSQPV 339

QY 76 P---PRPQSTKPEL-RELSRKIRENMNTISQESARVNHR 111

Db 340 PSPAPTPTMPNQTDREVEKRLREKEVRKEARRQSR 379

RESULT 2

A43906

nuclear phosphoprotein xnf7 - African clawed frog

C/Species: Xenopus laevis (African clawed frog)

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 11-Jan-2000

C/Accession: A43906; S27947

R/Reddy, B.A.; Kloc, M.; Eskin, L.

Dev. Biol. 148, 107-116, 1991

A/Title: The cloning and characterization of a maternally expressed novel zinc finger n

A/Reference number: A43906; MUID:92038424; PMID:1936552

A/Accession: A43906

A/Molecule type: mRNA

A/Residues: 1-609 <RED>

A/Cross-references: EMBL:M63705; NID:g214914; PID:g214915

A/Note: sequence extracted from NCBI backbone (NCBI:64515, NCBI:64520)

C/Genetics:
A/Gene: xnf7

C;Superfamily: Xenopus nuclear phosphoprotein xnf7; RING finger homology
C;Keywords: DNA binding; nucleus; phosphoprotein; zinc finger
F;141-190/Domain: RING finger homology <RNG>

Query Match 11.9%; Score 84.5; DB 2; Length 609;
Best Local Similarity 30.9%; Pred. No. 7.4;
Matches 30; Conservative 12; Mismatches 38; Indels 17; Gaps 4;

Qy	50	HEVLP-----GTGASAIATVTPKGASMKLPPRPQSTKPEL--REL-SRKIRFEMNKTISQ	103
		: : : :	
Db	255	HNFLPDLAVGVYRELSAIVAPLEASLKV-----TEQLSSQSDKIEQHNVQMSQ	305
Qy	104	ESARNHRLPEGHPLLEKRAEYFRHLRSLKSSQGVNRL	140
Db	306	YKEHTTSFEKLHKFLREREE--KLLEQLKQGGENLL	340

```

RESULT 3
S33981
vif protein - human immunodeficiency virus type 1
C Species: human immunodeficiency virus type 1, HIV-1
C Date: 19-Mar-1997 #ssequence_revision 19-Mar-1997 #text_change 20-Sep-1999
C Accession: S33981
R;Carlini, F.
submitted to the EMBL Data Library, November 1991
A;Reference number: S33979
A;Accession: S33981
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-192 <CAR>
A;Cross-references: EMBL:Z11530; NID:G60192; PID:G60195
C;Superfamily: AIDS vif protein

```

Query Match	11.6%	Score 82;	DB 2;	Length 192;
Best Local Similarity	28.8%	Pred No. 3.2;		
Matches 30; Conservative	9;	Mismatches	33;	Indels 32; Gaps 5;
Qy	22	FDVNRALLRVKSSERLAMLRLALAG-----MCHRVLPFGTGAAGAATAATVTPKGASM	72	
	:	: : :	:	:
	:	: : :	:	:
Db	112	FDCFSESAIR-----NAILGNVVVRUCEYQAQGNNKIGSLQYLALAAAITPK----	157	
Qy	73	KLKPPRQSTQSPRELRSRLREMNKTTISQESARVNHRLEPH	116	
Db	158	KIKPPLPSVTKLTEDR-----WNKPQTKGHRNHTM-NGH	192	

RESULT 4
AG2057
hypothetical protein all2013 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AG2057
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena PCC 7120
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG2057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-239 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA873712.1; PID:gl7131l03; GSFDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all2013

```
Query Match      11.6%; Score 82; DB 2; Length 239;
Best Local Similarity 26.9%; Pred. No. 4.1;
Matches 21; Conservative 16; Mismatches 39; Indels 2; Gaps 17;

Qy      61 IAAITVTKGASMKLKPPTQSTKPELSLRK--IREMNXYTISQESARVNHRLPGEHPL 118
||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
```

141 IAA SLTPNGCFWNA DPILPESPTLAEIYQAAEEWVSEQGSNFTEVRAKVGDSSPQGSYN 200

Qy 119 LEKRAEYFRHLSKSG 136
::|||

Db 201 PQQLATLDTHLQMLTKSG 218

RESULT 5

G83405
hypothetical protein PA1923 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: G83405
R;Scover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Latbig, K.; Li,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pat
A;Reference number: AB2950; MCID:20437337; PMID:10984043
A;Accession: G83405
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1281 <STO>
A;Cross-references: GB:AE004618; GB:AE004091; NID:G9947912; PIDN:AA05311.1; GSPDB:GN0
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA1923

	Query Match	11.5%; Score 81.5; DB 2; Length 1281;
	Best Local Similarity	28.5%; Pred. No. 33;
	Matches 35; Conservative	16; Mismatches 59; Indels 13; Gaps 5;
Qy	25 MREALLRVKSSR-LA----	MLRALGMCCHRRVLPGTGASAIATVTPKGASKMLKLRPRP 79
Dd	743 LRFOGLARELDQLADTGTLEALLAGLAGRFVAPGGGDPIRNQVPFSGRNLPFAF----	798
Qy	80 QSKTKSPRLSRSLRKIREMNKTTISQESARVNH--RLPEGHPLLEKRAFYFRHLRSLSQGV	137
Dd	799 EADKVPTPAAYACAAAFAGQLL--ESYRAEHQGAPEKLAFSLWSSTMRHLGIVESQAL	856
Qy	138 NRL 140	
b	857 HAL 859	

RESULT 6
S42996
viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1. HIV-1
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C:Accession: S42996
R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A:Description: In vivo genetic variability of the HIV-1 gene.
A:Reference number: S42940
A:Accession: S42996
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-192 <NIE>
A:Cross-references: EMBL:Z30687; NID:g459611; PIN:CAA83167.1; PID:g459612
C:Superfamily: AIDS vif protein

	Query Match	11.4%	Score 81;	DB 2;	Length 192;	
	Best Local Similarity	29.8%	Pred.No. 3.9;			
	Matches 31; Conservative	8;	Mismatches	33; Indels	32; Gaps	5;
Qy	22 FDVNRALLRVKSSERLAMIPLAAG-----MCHRRVLPGFGASAIATVTTPKGASM	72				
	: : :	:	:	:	:	:
Dd	112 FDCFSESAIR-----KALIGHTVSPSCRYAQGNKVGLQLYLAALAVTPK----	157				
	: : :	:	:	:	:	:
Qy	73 KKLPPRPQSTKSPELRSLSKIREMNNTISQESARVNHRLPPEGH	116				
	: : :	:	:	:	:	:
Dd	158 KTKPPLPSVTKLTEDR-----WNKPQRTKGHRENTHT-NGH	192				
	: : :	:	:	:	:	:

```
RESULT 7
C83328
hypothetical protein PA2548 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83328
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: C83328
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <STO>
A:Cross-references: GB:AE004682; GB:AE004091; NID:g9948598; PIDN:AAG05936.1; GSPDB:GN001
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA2548

Query Match 11.3%; Score 80; DB 2; Length 464;
Best Local Similarity 27.5%; Pred. No. 14;
Matches 36; Conservative 17; Mismatches 46; Indels 32; Gaps 7;

QY 20 ETDVMEALLRVKSSERLAMLALAGMCHRVLPCTGASAIATVTPKG-ASMKLK--- 75
DB 285 EDVPLGRRLLFLYDKGKPNWAQALV-----RFAQGPQGAI---VTRSGFVAQKIQAVQ 336
QY 76 -PPRPOSTKSPELRELSRKIREVNKKTISOESARVNHRLPEGHPLLEKRA-----EYF 126
DB 337 IAPRPQ--MFAEYKLAEQARLT-----VNFQEGSALLONKALLDVQRLLDYL 385
QY 127 RHLRLSKSQV 137
DB 386 RQNRKQERTV 396

RESULT 8
T49878
respiratory burst oxidase protein A - Arabidopsis thaliana
N:Alternate names: protein T211.100
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T49878
R:Bavan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Le
submitted to the Protein Sequence Database, April 2000
A:Reference number: 224493
A:Accession: T49878
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-902 <BEV>
A:Cross-references: EMBL:AL163912; GSPDB:GN00063; ATSP:T211.100
A:Experimental source: cultivar Columbia; BAC clone T211
C:Genetics:
A:Gene: ATSP:T211.100
A:Map position: 5
A:Introns: 180/1; 232/2; 248/3; 286/3; 428/3; 557/3; 589/3; 628/2; 662/3; 687/2; 867/1

Query Match 11.3%; Score 80; DB 2; Length 902;
Best Local Similarity 25.2%; Pred. No. 30;
Matches 37; Conservative 22; Mismatches 42; Indels 46; Gaps 7;

QY 3 STSTTNFVAENRPTFGTDFV-----MREALLRV-KSERLA 39
DB 31 NVATTSTNYGDEFPYVEITLIDHDSVSVYGLKSPNHRGAGSNVEDQSLLRQGRSGRSNS 90
QY 40 MLRALAGMCHRVLPCTGASAIATVTPKGASMKLKPPEPQSTK---SPELRELSRK-IR 95
DB 91 VLKRLASSV-----STGTRVASSVSSSSAR---KPPRPQLAKLRSSRAELAKGLK 141
```

```
QY 96 EMMKNTISOESARVNHRLPEGHPLLEKR 122
DB 142 FITKTDG-----VTGWPEVEKR 158
```

```
RESULT 9
T49799
related to TOM1 protein [imported] - Neurospora crassa
N:Alternate names: protein B11B22.10
C:Species: Neurospora crassa
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C:Accession: T49799
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatur
submitted to the Protein Sequence Database, May 2000
A:Reference number: 225022
A:Accession: T49799
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-3839 <SCH>
A:Cross-references: EMBL:AL356834; GSPDB:GN00116; NCSB:B11B22.10
A:Experimental source: BAC clone B11B22; strain OR74A
C:Genetics:
A:Gene: NCSB:B11B22.10
A:Map position: 6
A:Introns: 16/3; 2607/1; 2623/1; 2658/1; 2845/1; 2987/2; 3204/3; 3694/1; 3809/1
```

```
Query Match 11.2%; Score 79.5; DB 2; Length 3839;
Best Local Similarity 20.9%; Pred. No. 1.9e+02;
Matches 34; Conservative 26; Mismatches 50; Indels 53; Gaps 7;

QY 16 PTFGTFDVMREALLRVKSSER-----LAMLRALAGMCHRVLPCTGASAIATVTP 67
DB 3344 PTFGGMWCKLSACLSAIRQRDNMLNVAITLLPIESLMVCKNTTL--SDASAVSNANSQ 3401
QY 68 KCASMKLPPRPQS-----TKSPELRELSR 92
DB 3402 K--EMLLTSPPPEDRIAGLFTTTEHRIINELVRHNPKLMSTGTSLLVKNPKVLEFDN 3459
QY 93 KIREMNKTIISOESARVNHRLPEGHPL-LEKAEYFRH--LRSL 132
DB 3460 KENYENRSVHSKYQOTRHSFP---PLQLQVREHVPHDSFSL 3499
```

```
RESULT 10
S42944
viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C:Accession: S42944
R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A:Description: In vivo Genetic variability of the HIV-1 gene.
A:Reference number: S42940
A:Accession: S42944
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-192 <WIB>
A:Cross-references: EMBL:Z30605; NID:g459454; PIDN:CAA83082.1; PID:g459455
C:Superfamily: AIDS vif protein

Query Match 11.2%; Score 79; DB 2; Length 192;
Best Local Similarity 29.0%; Pred. No. 6;
Matches 31; Conservative 10; Mismatches 28; Indels 38; Gaps 6;

QY 22 FDVMEALLRVKSSERLAMLALAGMCHRVLPG-----TGA---SIAATVTPKG 69
DB 112 FCFPSDSAIR-----NAILGHRVSPSPCEYQAGHKVGSGLQYALALITPK- 157
QY 70 ASMKLKPPRPOSTKSPELRELSRKIREMNKTIISOESARVNHRLPEGH 116
DB 158 ---KIKPFLPSVTKLTEDR-----WNKPQKTKGRGSHTL-NGH 192
```

QY 4 TSTTTNFVAENRPTFGSETFDYMRALLRVKSSERLAMPALAGMCCHRVLPCTGSAIAA 633

QY	4	TSTTNFVAENRPTGCTFDVWREALLRVKSSERLAMLRLAGCMGHRVLPGTGASAI	AA 63
DB	997	TDTTTLRLVRLGWAYSDDEKVKVLKKAATEPRVW	-----HEPMEVFPTAFGA 1047
QY	64	TVTPKGSAMKLPFRPQSTKSPELRSLKIREMNKTI	SQ 103
DB	1048	STLDHELRLVLR	-----ELDRSRTVDELNRTIQ 1077
RESULT 17			
D95547	hypothetical protein F23H24.12 [imported] - Arabidopsis thaliana		
C:	Species: Arabidopsis thaliana (mouse-ear cress)		
C:	Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001		
C:	Accession: D96547		
R:	Phellogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso		
R:	Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Huizar, L.		
Nature	408, 816-820, 2000		
C:	A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.		
C:	A:Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani		
R:	Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.		
A:	Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,		
ket, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.			
A:	Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.		
A:	Reference number: A86141; MUID:21016719; PMID:11130712		
A:	Accession: D96547		
A:	Status: preliminary		
A:	Molecule type: DNA		
A:	Residues: 1-171 <STO>		
A:	Cross-references: GB:AE005173; NID:g1128410; PIDN:AAG31212.1; GSPDB:GN00141		
C:	Genetics:		
A:	Gene: F23H24.12		
A:	Map position: 1		
Query Match	11.0%;	Score 78;	DB 2; Length 171;
Best Local Similarity	28.4%;	Pred. No. 6.4;	
Matches	25; Conservative	13; Mismatches	18; Indels 32; Gaps 4;
QY	81	STKSPELRSLKIREMNKTI	-----QESRVNHLRPGHP----- 117
DB	7	TSESTFEELCREBITQNDIONLVRENAQLNH	-----PIGRPYFDAIEEVRKXNDKRMKLQ 64
QY	118	LLEKRAEYFR	-----HLRSLKSQGV 138
DB	65	ELYEKKEVWKKEKTFHLKSLRKQMAN	92
RESULT 18			
S42959	viral infectivity factor vif - human immunodeficiency virus type 1		
C:	Species: human immunodeficiency virus type 1, HIV-1		
C:	Date: 06-Feb-1995 #sequence_revision 05-Feb-1995 #text_change 20-Sep-1999		
C:	Accession: S42959		
R:	Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.B.		
A:	Description: In vivo genetic variability of the HIV-1 gene.		
A:	Reference number: S42940		
A:	Accession: S42959		
A:	Status: preliminary		
A:	Molecule type: DNA		
A:	Residues: 1-192 <WIE>		
A:	Cross-references: EMBL:Z30620; NID:g459482; PIDN:CAA83087.1; PID:g459483		
C:	Superfamily: AIDS vif protein		
Query Match	11.0%;	Score 78;	DB 2; Length 192;
Best Local Similarity	30.5%;	Pred. No. 7.4;	
Matches	29; Conservative	10; Mismatches	42; Indels 14; Gaps 4;
QY	22	FDVWREALLRVKSSERLAMLRLAGCMGHRVLPGTGASAI	AAVTVPKGSAMKLPFRPQ 81
DB	112	FDGFSSEISATVGRIVSPRC	-----EYQAGHNKVSQLOYLALAAITPK-----KIKPPJPSV 166

DB 130 AQLGEVQHLMTVQ 143

RESULT 21

ASLJS3

vif protein - human immunodeficiency virus type 1
 N;Alternate names: orf-Q protein; sor protein
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 17-May-1985 #sequence_revision 31-Mar-1993 #text_change 16-Jul-1999
 C;Accession: A04002; A36757; A36756; A36765; S42971
 R;Arya, S.K.; Gallo, R.C.
 Proc. Natl. Acad. Sci. U.S.A. 83, 2209-2213, 1986
 A;Title: Three novel genes of human T-lymphotropic virus type III: immune reactivity of
 A;Reference number: A94093; MUID:86177573; PMID:3008154
 A;Accession: A04002
 A;Molecule type: DNA
 A;Residues: 1-192 <ARY>
 A;Cross-references: GB:M11840; NID:g328453; PIDN:AAA44997.1; PID:g328454
 A;Experimental source: isolate HTLV-III, 12
 R;Ratner, L.A.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Dor
 nberger, J.A.; Papas, T.S.; Ghayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
 Nature 313, 277-284, 1985
 A;Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
 A;Reference number: A93353; MUID:85111123; PMID:2578615
 A;Accession: A36757
 A;Molecule type: DNA
 A;Residues: 1-192 <RAT>
 A;Cross-references: GB:M15654; NID:g326383; PIDN:AAA44202.1; PID:g326389
 A;Experimental source: isolate HTLV-III, BH10
 R;Main-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
 Cell 40, 9-17, 1985
 A;Title: Nucleotide sequence of the AIDS virus, LAV.
 A;Reference number: A90866; MUID:85099333; PMID:2981635
 A;Accession: A36756
 A;Molecule type: DNA
 A;Residues: 1-192 <WAI>
 A;Cross-references: GB:K02013; NID:g326417; PIDN:AAB59748.1; PID:g326421
 A;Experimental source: isolate LAV-1a
 R;Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Laeky, L.A.; Capon, D.J.
 Nature 313, 450-458, 1985
 A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov
 A;Reference number: A93355; MUID:85111157; PMID:2982104
 A;Accession: A36765
 A;Molecule type: DNA
 A;Residues: 1-192 <MUE>
 A;Cross-references: GB:X01762
 A;Experimental source: isolate IV
 R;Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.B.
 Submitted to the EMBL Data Library, March 1994
 A;Description: In vivo genetic variability of the HIV-1 gene.
 A;Reference number: S42940
 A;Accession: S42971
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-192 <WIE>
 A;Cross-references: EMBL:Z30632; NID:g459506; PIDN:CAA83109.1; PID:g459507
 C;Genetics:
 C;Gene: vif
 C;Superfamily: AIDS vif protein
 C;Keywords: AIDS; immunodeficiency

Query Match 10.9%; Score 77; DB 1; Length 192;
 Best Local Similarity 27.9%; Pred. No. 9.1;
 Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

QY 22 FDVWRALLRVKSSERLAMLALAG-----KALLGHVSPRCEYQAGHNVKVSLOYLALALITPK----- 157

DB 112 FDCFSDAIR-----KALLGHVSPRCEYQAGHNVKVSLOYLALALITPK----- 157

QY 73 KLXPPRPQSTKSPPELRSLRKTREMNKTTISQESARVNHRLPEGH 116

DB 158 KIKPPLPSVTKLTEDR-----WNKPKTKGHRGSHM-NGH 192

DB 82 TYSPELRSLRKIREMNKTTISQESARVNHRLPEGH 116

DB 167 TKLTEDR-----WNKPKTKGHRGSHM-TGH 192

RESULT 19

F72655

hypothetical protein APE0673 - Aeropyrum pernix (strain K1)
 C;Species: Aeropyrum pernix
 C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
 C;Accession: F72655
 R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Jin-no, K.; Takah
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
 DNA Res. 6, 83-101, 1999
 A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
 A;Reference number: A72450; MUID:99310339; PMID:10382966
 A;Accession: F72655
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-686 <KAW>
 A;Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79646.1; PID:d1043432; PID:g510
 A;Experimental source: strain K1
 C;Genetics:
 A;Gene: APE0673

Query Match 11.0%; Score 78; DB 2; Length 686;
 Best Local Similarity 25.4%; Pred. No. 33;
 Matches 30; Conservative 15; Mismatches 39; Indels 34; Gaps 4;

QY 49 GHRVLPGTCASAIATVTPKPGASMLKPPRPOSTKSPPELRSLRKI-----REM 97

DB 175 GLAAVPSGGSVVAVAPKGLSKI-----SPILRLNLSIYTPPGVPGSPREA 225

QY 98 NKTISQESARVNHRLPEGHLLPEKR-----AEY-----FRLRLSKSQGVNRLI 141

DB 226 MEYIRGEKARLGRRLVSIQEMASERLIGELAEFTVVTAFENIFKELVSTLARGETRIV 283

RESULT 20

A45339

outer capsid protein VP5 - Broadhaven virus
 C;Species: Broadhaven virus
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 23-Jul-1999
 C;Accession: A45339
 R;Voss, S.R.; Fukusho, A.; Nuttall, P.A.
 Virology 179, 482-484, 1990
 A;Title: RNA segment 5 of Broadhaven virus, a tick-borne orbivirus, shows sequence homol
 A;Reference number: A45339; MUID:91021056; PMID:2171220
 A;Accession: A45339
 A;Molecule type: genomic RNA
 A;Residues: 1-480 <MOS>
 A;Cross-references: GB:M58030; NID:g210813; PIDN:AAA42802.1; PID:g210814
 C;Genetics:
 A;Map position: segment 5
 C;Superfamily: bluetongue virus outer capsid protein VP5
 C;Keywords: capsid protein; coat protein; glycoprotein
 F;122,201/Binding site: carbohydrate (Asn) #status predicted

Query Match 10.9%; Score 77.5; DB 1; Length 480;
 Best Local Similarity 24.6%; Pred. No. 24;
 Matches 33; Conservative 22; Mismatches 60; Indels 19; Gaps 5;

QY 14 NRTFTGETDVNREALLRVKSSERLAMLALAGMCHRVLPQT--GASAIATVTPKQAS 71

DB 15 NRIGSGITTAARSDDTTTKRIPSAAGRAVERVAASEIGQRAIGWEGAATAALTGESVGES 74

QY 72 MK-----LKPPRPQSTKSPPELRSLRKTREMNKTTISQESARVNHRLPEGHLLPEKR 122

DB 75 VKRAVILNVAGVHQVTPDPLNPVEI--ETQAKRLDLANKREAQIRH-----NKSMLQKE 129

QY 123 AEYF-----RHLRSUK 133

RESULT 22

ASLUNA
vif protein - human immunodeficiency virus type 1 (isolate NIT-A)
N:Alternate names: orf-Q protein; sor protein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 31-Jan-1997
C:Accession: A41308
R:Sakai, K.; Ma, X.; Gordienko, I.; Volsky, D.J.
J. Virol. 65, 5765-5773, 1991
A:Title: Recombinational analysis of a natural noncytopathic human immunodeficiency virus
A:Reference number: A41308; MUID:92015467; PMID:1920615
A:Accession: A41308
A:Molecule type: DNA
A:Residues: 1-192 <SAK>
C:Genetics:
A:Gene: vif
C:Superfamily: AIDS vif protein
C:Keywords: AIDS; immunodeficiency

Query Match 10.9%; Score 77; DB 1; Length 192;
Best Local Similarity 27.9%; Pred. No. 9.1;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;
QY 22 FDMREALLRVKSSERLAMLRLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157
QY 73 KLPKPPQSTKSPPELRSKIREMNKTIQSASRVNHRHLEPEGH 116
Db 158 KIKPPLPSVTKLTEDR-----WNKPQKTGHRGSHTM-NGH 192

RESULT 23

S42964
viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C:Accession: S42964
R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A:Description: In vivo genetic variability of the HIV-1 gene.
A:Reference number: S42964
A:Accession: S42964
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-192 <WIE>
A:Cross-references: EMBL:Z30625; NID:g459492; PIDN:CAA83102.1; PID:g459493
C:Superfamily: AIDS vif protein

Query Match 10.9%; Score 77; DB 2; Length 192;
Best Local Similarity 27.9%; Pred. No. 9.1;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;
QY 22 FDMREALLRVKSSERLAMLRLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157
QY 73 KLPKPPQSTKSPPELRSKIREMNKTIQSASRVNHRHLEPEGH 116
Db 158 KIKPPLPSVTKLTEDR-----WNKPQKTGHRGSHTM-NGH 192

RESULT 24

S42960
viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C:Accession: S42960
R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A:Description: In vivo genetic variability of the HIV-1 gene.

A:Reference number: S42940

A:Accession: S42960
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-192 <WIE>
A:Cross-references: EMBL:Z30621; NID:g459484; PIDN:CAA83098.1; PID:g459485
C:Superfamily: AIDS vif protein

Query Match 10.9%; Score 77; DB 2; Length 192;
Best Local Similarity 27.9%; Pred. No. 9.1;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;
QY 22 FDMREALLRVKSSERLAMLRLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157
QY 73 KLPKPPQSTKSPPELRSKIREMNKTIQSASRVNHRHLEPEGH 116
Db 158 KIKPPLPSVTKLTEDR-----WNKPQKTGHRGSHTM-NGH 192

RESULT 25

S42940
viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C:Accession: S42940
R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A:Description: In vivo genetic variability of the HIV-1 gene.
A:Reference number: S42940
A:Accession: S42940
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-192 <WIE>
A:Cross-references: EMBL:Z30601; NID:g459446; PIDN:CAA83078.1; PID:g459447
C:Superfamily: AIDS vif protein

Query Match 10.9%; Score 77; DB 2; Length 192;
Best Local Similarity 30.5%; Pred. No. 9.1;
Matches 29; Conservative 9; Mismatches 43; Indels 14; Gaps 4;
QY 22 FDMREALLRVKSSERLAMLRLALAGMCGHRVLPGTGASAIATVTPKGASMKLKPDPPOS 81
Db 112 FDCFSESARKAIVGLVNPNC-EYLAGHNKVGSLQYLALALITPK-----KIKPPLPSV 166
QY 82 TKSPPELRSKIREMNKTIQSASRVNHRHLEPEGH 116
Db 167 RKLTEDR-----WNKPQKTGHRGSHTM-NGH 192

RESULT 26

S42946
viral infectivity factor vif - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C:Accession: S42946
R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A:Reference number: S42940
A:Accession: S42946
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-192 <WIE>
A:Cross-references: EMBL:Z30607; NID:g459458; PIDN:CAA83084.1; PID:g459459
C:Superfamily: AIDS vif protein

Query Match 10.9%; Score 77; DB 2; Length 192;
Best Local Similarity 27.9%; Pred. No. 9.1;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;
QY 22 FDMREALLRVKSSERLAMLRLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72

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Db 112 FDCSDSAIR-----KALLGHIVSPRCEYQAGHNVKGSLOYLALAAALTPK----- 157
Qy 73 KKKPPRPOSTKSPELRSKIREMNTKISQESARVNHRLPEGH 116
Db 158 KKKPPLESVTKLTEDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 27
H84506
Probable retroelement pol polyprotein [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C/Accession: H84506
R/Lit, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umavam, L.; Tallon, L.;
cuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: H84420; MUID:20083487; PMID:10617197
A/Accession: H84506
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-889 <STO>
A/Cross-references: GB:AB020093; NID:94417309; PIDN:AAD20433.1; GSPDB:GN00139
C/Genetics:
A/Gene: At2g13330
A/Map position: 2

Query Match 10.9%; Score 77; DB 2; Length 889;
Best Local Similarity 26.8%; Pred. No. 55;
Matches 26; Conservative 17; Mismatches 46; Indels 8; Gaps 1;

Qy 20 ETDVMEALLRVKSSERLAMLRLAGMCGHRVLPGTGASAIATVTPKGASMKLPPRP 79
Db 744 ESKFLTRIPGENTSADTLAALASTDPFVKRIIPVEGIEHTSIDLVKVGAGMEPEAPP 803

Qy 80 QSTKSPELRSKIREMNTK-----TISQESARV 108
Db 804 QLELSRQLRRQVRQKRSQNKFRKLSMMVINEAKV 840

RESULT 28
S42977
viral infectivity factor vif - human immunodeficiency virus type 1
C/Species: human immunodeficiency virus type 1_HIV-1
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
C/Accession: S42977
R/Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
submitted to the EMBL Data Library, March 1994
A/Description: In vivo genetic variability of the HIV-1 gene.
A/Reference number: S42940
A/Accession: S42977
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-192 <WIE>
A/Cross-references: EMBL:230639; NID:9459520; PIDN:CAA83116.1; PID:9459521
C/Superfamily: AIDS vif protein

Query Match 10.7%; Score 76; DB 2; Length 192;
Best Local Similarity 28.0%; Pred. No. 11;
Matches 30; Conservative 11; Mismatches 28; Indels 38; Gaps 6;

Qy 22 FDMVREALLRVKSSERLAMLRLAGMCGHRVLP-----TGA---SAIAATVTPKG 69
Db 112 FDCSESAR-----SAILGHRVSPCEYQAGHNVKGSLOYLALAAALTPK- 157

Qy 70 ASMKLPPRPOSTKSPELRSKIREMNTKISQESARVNHRLPEGH 116
Db 158 ---KINPLPISKLTEDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 29
E95966
Probable aldehyde or xanthine dehydrogenase, molybdopterin binding subunit protein [im]
C/Species: Sinorhizobium meliloti
C/Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C/Accession: E95966
R/Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hern
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A/Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing en-
A/Reference number: A95842; MUID:21396508; PMID:11481431
A/Accession: E95966
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-325 <KUR>
A/Cross-references: GB:AL591985; PIDN:CAC49397.1; PID:G15140883; GSPDB:GN00167
A/Experimental source: strain 1021, megaplasmid pSymB
R/Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Huble,
Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A/Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaun-
hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, F.
A/Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A/Reference number: A96039; MUID:21368234; PMID:11474104
A/Contents: annotation
C/Genetics:
A/Gene: Smb21557
A/Genome: plasmid

Query Match 10.7%; Score 76; DB 2; Length 325;
Best Local Similarity 26.6%; Pred. No. 21;
Matches 33; Conservative 11; Mismatches 42; Indels 38; Gaps 5;

Qy 37 RLAMRLALAGMCGHRVLPOTGASAI-----AAVTPKGASM 72
Db 115 RCFYFMLDAPCNKRV-PGSGCSAIDGLNAGHAILGTSEHCVAITHPSDLAVSLVALGANL 173

Qy 73 KKKPPRPOSTKSPELRSKIREMNTKISQESARVNHRLPEGHPLLE---KRAEYFRHL 129
Db 174 SLKGPAGERTIPVE---ELFR-----LPSTPHLEHTLEPGELIVEVHPNGPYARKA 223

Qy 130 RSLK 133
Db 224 RYLK 227

RESULT 30
E82992
Probable FAD-dependent monooxygenase PA5221 [imported] - Pseudomonas aeruginosa (strain
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C/Accession: E82992
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; E
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lin
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: E82992
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-405 <STO>
A/Cross-references: GB:AE004935; GB:AE004091; NID:99951526; PIDN:AAG08606.1; GSPDB:GN00
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA5221
C/Superfamily: ubiH protein

Query Match 10.7%; Score 76; DB 2; Length 405;
Best Local Similarity 23.2%; Pred. No. 27;
Matches 23; Conservative 19; Mismatches 39; Indels 18; Gaps 3;

Qy 45 AGMCGHRV---LPGTGASAIATVTPKGASMKLPPRPOSTKSPELRSKIREMNTKI 101

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Db 10 AGMVGSALALALEGSGUEVLV-----DGGSLDVAPFKPEAPYPRV-----SAL 54
QY 102 SQESARNVHRLPEGHPLLEKRAEYFRHLRLSLKSGQVNL 140
Db 55 SEASRRILQRLHWDGIVARAEFYREMQVWDGSGTGRI 93

RESULT 31
G70522
C:Species: Mycobacterium tuberculosis (strain H37RV)
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: G70522
R:Coile, S.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: G70522
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-408 <COL>
A:Cross-references: GB:297188; GB:AL123456; NID:93261805; PIDN:CAB10011.1; PID:g2224818
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv3827c
C:Superfamily: hypothetical protein bl432

Query Match 10.7%; Score 76; DB 2; Length 408;
Best Local Similarity 30.6%; Pred. No. 27;
Matches 33; Conservative 11; Mismatches 44; Indels 20; Gaps 5;

QY 49 CHVLPGTGSASATVTPKGASMKLP-PPPOSTKSPRL-----ELSRKIREM 97
Db 218 GSRVGDVGVRLATVANAGVLEEVPNRPDLTALKELYASRARSCTKGSRRYR 277
QY 98 NKTIQSARVN-----HRLPEGHPLLEKRAEYFRHL--RSLKSGQVNR 139
Db 278 TTISRLHRRVNDVRTHL---HVLITRLAQTGHVVEGLDAGMLR 322

RESULT 32
I49603
transcription regulator - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49603
R:Galera, P.; Musso, M.; Ducy, P.; Karsenty, G.
Proc. Natl. Acad. Sci. U.S.A. 91, 9372-9376, 1994
A:Title: c-Krox, a transcriptional regulator of type I collagen gene expression, is predicted to be a myocyte enhancer factor-1-related protein
A:Reference number: I49603; MUID:95023913; PMID:793772
A:Accession: I49603
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-427 <RES>
A:Cross-references: GB:L35307; NID:9529399; PIDN:AAA61956.1; PID:9529400
C:Genetics:
A:Gene: c-Krox

Query Match 10.7%; Score 76; DB 2; Length 427;
Best Local Similarity 25.0%; Pred. No. 29;
Matches 35; Conservative 15; Mismatches 50; Indels 40; Gaps 7;

QY 32 VKSSERLMLRALAGMCHRVLPGTGASA-----IAATVT-----p 67
Db 4 VLQARLLLEIPCIVIAAC-MEILQSGGLEAPSPDEDDCERARQVLEAFATATTASTSGMP 62
QY 68 KG----ASWKLKPPRQSTKSPRLRELSKIREMNTISQ-ESARNVHRLPEG-----HP 117
Db 63 NGEDSPQVPLPLPPP-----PPPRVARSRRKPRKAFLOTQKGRANHLVPEAPTTLTHP 117

QY 118 LLEKRAEYFRHLRLSLKSGQV 137
Db 118 LTYEEEMVGRNLNGSGGSL 137

RESULT 33
G75403
DNA topoisomerase I - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: G75403
R:White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: G75403
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1021 <WHI>
A:Cross-references: GB:AE001983; GB:AE000513; NID:96459123; PIDN:AAF10943.1; PID:964591
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1374
A:Map position: 1
C:Superfamily: bacterial type I DNA topoisomerase

Query Match 10.7%; Score 76; DB 2; Length 1021;
Best Local Similarity 28.2%; Pred. No. 80;
Matches 37; Conservative 20; Mismatches 40; Indels 34; Gaps 7;

QY 28 ALLRVKSSERLMLRALAGMCHRVLPQTG-----ASAIATVTPKGASMKL----- 74
Db 267 ARLTEVQGERLAAGKDFDLTG-QLRPGAGVRLLEGEALAIASEGLKQTLKVLTAEEKP 325
QY 75 ---KPPRQSTKSPRLRELSKIREMNTISOESARNVHRLPEGHPLLEKRAEYFRHL- 130
Db 326 FTSRPPAPFITSILO-QEGSRKLR---MSAQTMTRTAQRLYEG-----GYITYMRT 372
QY 131 ---SLKSGQVNR 138
Db 373 DSTNLSSBAVN 383

RESULT 34
F97169
static acid synthase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C:Accession: F97169
R:Noelling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium C. acetobutylicum
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: F97169
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-350 <KUR>
A:Cross-references: GB:AE001437; PIDN:AAK80145.1; PID:g15025193; GSPDB:GN00168
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC2187
C:Superfamily: Streptococcus agalactiae capsular polysaccharide biosynthesis protein cp

Query Match 10.7%; Score 75.5; DB 2; Length 350;
Best Local Similarity 27.1%; Pred. No. 25;
Matches 32; Conservative 14; Mismatches 45; Indels 27; Gaps 4;

QY 20 ETFDVMREALLRVKSSERLMLRALAGMCHRV--LPQTGASAIATVTPKGASMKLPP 77
Db 200 KTFPNMREA-----FNCSVGLSDHTMGYSVATAAVALGATVIEKHFILKSDG 247
```

QY 78 RPOSTKSPPELRLS-----RKIREMKNKTIQSARVNHRLPEGHPLLEKRAEYFRHLRSL 132
 Db 248 GPDARSMPPEFSAMVKSIREVEKALGKVT-----YELTEKQKNSQHSRSL 295

RESULT 35
 S43000
 C:Species: human immunodeficiency virus type 1
 C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
 C:Accession: S43000
 R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
 submitted to the EMBL Data Library, March 1994
 A:Description: In vivo genetic variability of the HIV-1 gene.
 A:Reference number: S42940
 A:Accession: S43000
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-192 <WIE>
 A:Cross-references: EMBL:Z30691; NID:G459619; PIDN:CAA83171.1; PID:G459620
 C:Superfamily: AIDS vif protein

Query Match 10.6%; Score 75; DB 2; Length 192;
 Best Local Similarity 27.1%; Pred. No. 14;
 Matches 29; Conservative 9; Mismatches 31; Indels 38; Gaps 5;

QY 22 FDMREALRVKSSERLAMLALAGMCHRVLP-----GTGASATAATVTPKG 69
 Db 112 FDCFSASIR-----QALGHRVSPCEYRAGHNKVGSLQYLAALVTPK- 157

QY 70 ASMKLPPRPQSTKSPELRLSKIREMKNKTIQSARVNHRLPEGH 116
 Db 158 ---KIKPPLPSVTKLTEDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 36
 S42965
 C:Species: human immunodeficiency virus type 1
 C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 20-Sep-1999
 C:Accession: S42965
 R:Wieland, U.; Hartmann, J.; Suhr, H.; Salzberger, B.; Eggers, H.J.; Kuehn, J.E.
 submitted to the EMBL Data Library, March 1994
 A:Description: In vivo genetic variability of the HIV-1 gene.
 A:Reference number: S42940
 A:Accession: S42965
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-192 <WIE>
 A:Cross-references: EMBL:Z30626; NID:G459494; PIDN:CAA83103.1; PID:G459495
 C:Superfamily: AIDS vif protein

Query Match 10.6%; Score 75; DB 2; Length 192;
 Best Local Similarity 29.0%; Pred. No. 14;
 Matches 31; Conservative 9; Mismatches 29; Indels 38; Gaps 6;

QY 22 FDMREALRVKSSERLAMLALAGMCHRVLP-----TGA---SATAATVTPKG 69
 Db 112 FDCFSASIR-----NALGHRVSPCEYQAGHNKVGSLQYLAALVTPK- 157

QY 70 ASMKLPPRPQSTKSPELRLSKIREMKNKTIQSARVNHRLPEGH 116
 Db 158 ---KIKPPLPSVAKLTEDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 37
 G75302
 C:Species: 5'-phosphate decarboxylase - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: G75302
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: G75302
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-606 <WHI>
 A:Cross-references: GB:AE002053; GB:AE000513; NID:G645999; PIDN:AAF11749.1; PID:G64600
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2200
 A:Map position: 1

Query Match 10.6%; Score 75; DB 2; Length 606;
 Best Local Similarity 26.0%; Pred. No. 53;
 Matches 33; Conservative 20; Mismatches 58; Indels 16; Gaps 5;

QY 13 ENRP-----TGGETFDMREALRVKSSERLAMLALAG-MCHRVLP-GTGASIAATVTT 66
 Db 81 EQRPQFPQFVFRQRTGLRAKQOVKVEQPRQPAAGGVVVGQVHPVVGQAAVAP-R 139

QY 67 PKGASMKLKPPRPOSTK---SPELRLSKIREMKNKTIQSARVNHRLPEGHPLLEKRA 123
 Db 140 PRAQRRRLPAPVAARLVPCPQRQQTAGERQLVPLPCPHRVQHARPGEDVALN--- 196

QY 124 EYFRHLR 130
 Db 197 ---RHVR 200

RESULT 38
 A48467
 C:Species: Brugia malayi
 C>Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 13-Feb-1998
 C:Accession: A48467
 R:Dissanayake, S.; Xu, M.; Pleskens, W.F.
 Mol. Biochem. Parasitol. 56, 349-351, 1992
 A:Title: Myosin heavy chain is a dominant parasite antigen recognized by antibodies in
 A:Reference number: A48467; MUID:93133225; PMID:1484558
 A:Accession: A48467
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-1313 <DIS>
 A>Note: sequence inconsistent with the nucleotide translation
 A>Note: sequence extracted from NCBI backbone (NCBIN:122784; NCBI:P:122786)
 C:Superfamily: myosin heavy chain; myosin motor domain homology
 C:Keywords: ATP

Query Match 10.6%; Score 75; DB 2; Length 1313;
 Best Local Similarity 27.0%; Pred. No. 1.3e+02;
 Matches 20; Conservative 15; Mismatches 33; Indels 6; Gaps 1;

QY 73 KKLPPRPOSTKSPELRLSKIREMKNKTIQSARVNHRLPEGHPLLEKRAEYFRHLRSL 132
 Db 199 KIKPMLKCGEGEIEKMNQIKELKENIANEEKARLESNTKLLERNNVNFLEAA 258

QY 133 KSQ-----GVNRL 140
 Db 259 KAQLSDVDDRLNRL 272

RESULT 39
 A45627
 C:Species: Brugia malayi
 C:Species: Brugia malayi
 C>Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 02-Feb-2001
 C:Accession: A45627; B45526
 R:Werner, C.; Rajan, T.V.
 Mol. Biochem. Parasitol. 50, 261-268, 1992
 A:Title: Characterization of a myosin heavy chain gene from Brugia malayi.

	Query Match	10.5%	Score 74.5	DB 2	Length 288
	Best Local Similarity	26.3%	Pred. No. 25		
	Matches 30	Conservative	23	Mismatches 42	Indels 19
					Gaps 6
Qy	16	PTGETFDVNRALLRVKSSERLALRALAGMGCHRV	-----LP-----	GTGCSAIAAT	64
Db	8	PETGFNFAYLDE---	QTKRSIRRALIKAVX-I	IPGHQIPFSSREPMPSYMGVGTGCIQVTAA	63
Qy	65	VTPKGASMK-LKPPRPOSTKSPSELRELRSKIRENMKNTISQESA---	RVNHLRPE	114	
Db	64	VIGOTDVLKVIDOGADTTNAVNIIRFFQKVCVGKTTSTQAAATLLQTHRRIE	117		

Search completed: November 14, 2003, 10:42:34
Job time : 44 secs

OM protein - protein search, using sw model

Run on: November 14, 2003, 10:38:30 ; Search time 37 Seconds

(without alignments)
179,210 Million cell updates/sec

Title: US-10-087-573-2

Perfect score: 708

Sequence: 1 MESTSTTNFVAENRPTGE.....RAEYFRHLRLSLKSGVNRLL 141

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	82	11.6	700	1	TRDN_CANFA
2	78.5	11.1	1120	1	KEPA_ECOLI
3	78	11.0	686	1	VAT1_AERPE
4	77.5	10.9	480	1	VP5_ERD
5	77	10.9	192	1	VIF_HV1B1
6	77	10.9	192	1	VIF_HV1NA
7	76	10.7	192	1	VIF_HV1B5
8	74.5	10.5	400	1	DH12_RAT
9	74	10.5	662	1	TLPB_BACSU
10	74	10.5	908	1	VP2_ERD
11	73.5	10.4	429	1	VIOC_HALUSQ
12	73.5	10.4	437	1	YGY3_HALUSQ
13	73.5	10.4	1187	1	PTNE_HUMAN
14	73	10.3	109	1	VIF_HV1SC
15	73	10.3	666	1	FLID_VIBCH
16	72	10.2	642	1	PHSA_STRAT
17	72	10.2	1805	1	HMW2_MYCGE
18	72	10.2	3259	1	GIAN_HUMAN
19	71.5	10.1	212	1	NUIM_BOVIN
20	71.5	10.1	392	1	PGK_NEIMA
21	71.5	10.1	392	1	PGK_NEIMA
22	71.5	10.1	559	1	Y876_MYCTU
23	71.5	10.1	732	1	Y8K8_YEAST
24	71.5	10.1	748	1	CIAT_HUMAN
25	71.5	10.1	2564	1	SFCO_HUMAN
26	71	10.0	192	1	VIF_HV1RH
27	71	10.0	211	1	HIT_PIG
28	71	10.0	377	1	HSF7_ARATH
29	71	10.0	411	1	APGM_PYRAB
30	71	10.0	411	1	APGM_PYRUF
31	71	10.0	1061	1	RNE_ECOLI
32	71	10.0	1189	1	PTNE_MOUSE
33	70.5	10.0	570	1	ZDS_FAIZE

ALIGNMENTS

RESULT 1

ID	TRDN_CANFA	STANDARD	PRT	700 AA
AC	P82179			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Triadin.			
GN	TRDN.			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
OX	NCBI_TaxID=9615;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.			
RC	TISSUE=Heart, and Skeletal muscle;			
RX	MEDLINE=99428545; PubMed=10497235;			
RA	Kobayashi Y.M., Jones L.R.;			
RT	"Identification of triadin 1 as the predominant triadin isoform expressed in mammalian myocardium";			
RL	J. Biol. Chem. 274:28660-28668(1999).			
CC	!- FUNCTION: MAY BE INVOLVED IN ANCHORING CALSEQUESTIN TO THE JUNCTIONAL SARCOPLASMIC RETICULUM AND ALLOWING ITS FUNCTIONAL COUPLING WITH THE RYANODINE RECEPTOR (BY SIMILARITY).			
CC	!- SUBCELLULAR LOCATION: Type II membrane protein. Sarcoplasmic reticulum.			
CC	!- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=3;			
CC	Name=Skeletal;			
CC	ISOID=P82179-1; Sequences=Displayed;			
CC	Name=Cardiac 1;			
CC	ISOID=P82179-2; Sequence=VSP_004001; VSP_004002;			
CC	Name=Cardiac 3;			
CC	ISOID=P82179-3; Sequence=VSP_004003; VSP_004004;			
CC	!- TISSUE SPECIFICITY: SKELETAL AND CARDIAC MUSCLE.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			

DR	EMBL; AF165916; AAF00222.1; ..			
DR	EMBL; AF165915; AAF00221.1; ..			
DR	EMBL; AF165917; AAF00223.1; ..			
DR	Transmembrane; Sarcoplasmic reticulum; Glycoprotein; Alternative splicing.			
KW	INIT_MET 1 0 0 BY SIMILARITY.			
FT	DOMAIN 1 46 CYTOPLASMIC (POTENTIAL).			
FT	TRANSMEM 47 67 POTENTIAL.			
FT	DOMAIN 68 700 LUMENAL (POTENTIAL).			
FT	CARBOHYD 74 74 N-LINKED (GLCNAC...).			
FT	CARBOHYD 616 616 N-LINKED (GLCNAC...).			
FT	VARSPLIC 257 277 DQYAFRCYRIMDFVHGDLRPG -> GKHSSEVAGGSKRTLG (POTENTIAL).			

Q13428 homo sapien
P16688 escherichia
P79145 canis famil
P24797 gallus gall
P47037 saccharomyc
P07208 trypanosoma
P51834 bacillus su
P11047 homo sapien
P13733 homo sapien
Q01397 neurospora
P21111 homo sapien
Q50538 methanosarc

FT KQIQ (in isoform Cardiac 1).
FT /FTId=VSP 004001.
FT Missing (in isoform Cardiac 1).
FT /FTId=VSP 004002.
FT /FTId=VSP 004003.
FT E -> EPIKGVKVPGLKEKE (in isoform
FT Cardiac 3).
FT /FTId=VSP 004003.
FT EEPVQVQVATEKAAIEKTKVPKPAKHAHQKESPTIKTD
FT KKPPTSKEPTVES -> GILQVPEVNLCLFLVQFOQDE
FT ELNVESKVFPMHVLHSHPTSRTSPILVISTTCT (in
FT isoform Cardiac 3).
FT /FTId=VSP 004004.
FT /FTId=VSP 004005.
SQ SEQUENCE 700 AA; 78152 MW; F033E3AA1BEE0C56 CRC64;

Query Match 11.6%; Score 82; DB 1; Length 700;
Best Local Similarity 27.4%; Pred. No. 7.1;
Matches 26; Conservative 15; Mismatches 34; Indels 20; Gaps 2;

QY 56 TGASATAATVTPKA-----SMKLKPPPOSTKSPELRELSRKIRENMKTISOE 104
DB 534 TEKAAIEKTVKPAKHAHQKESPTIKTDKPKTSKETPTVESGKKIKESKESKE 593
QY 105 SARVNRHLPEGHPLLEKRAEYFRHLRLSLKSGQVNR 139
DB 594 KAEMKHL-----KEEKVSTRKESLQSHNVTK 619

RESULT 2
KEFA_ECOLI
ID KEFA_ECOLI STANDARD; PRT; 1120 AA.
AC P773B;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Potassium efflux system KefA (AefA protein).
GN KEFA OR AEFB OR B0465.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R.; Plunkett G. III; Bloch C.A.; Perna N.T.; Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RN Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis K.,
RA Duncan M., Federspiel N., Hyman R., Kaiman S., Komp C., Kurqi O.,
RA Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99219852; PubMed=10202137;
RA Levine N., Totemeyer S., Stokes N.R., Louis P., Jones M.A.,
RA Booth I.R.;
RT "Protection of Escherichia coli cells against extreme turgor by
RT activation of MscS and MscL mechanosensitive channels: identification
RT of genes required for MscS activity";
RL EMBL J 18:1730-1737(1999).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE UPF0003 FAMILY.

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CC -----
DR EMBL; Y07802; CRA69140.1; -;
DR EMBL; AE000152; AAC73567.1; -;
DR EMBL; U82664; AAB40219.1; -;
DR PIR; H64776; H64776;
DR EcGene; EG14240; kefA.
DR InterPro; IPR006686; MS_channel_dom.
DR InterPro; IPR006685; MSion_channel.
DR Pfam; PF00924; MS_channel; 1.
DR PROSITE; PS01246; UPF0003; 1.
KW Transmembrane; Inner membrane; Transport; Potassium transport;
KW Complete proteome.
FT TRANSMEM 13 33 POTENTIAL.
FT TRANSMEM 500 520 POTENTIAL.
FT TRANSMEM 561 581 POTENTIAL.
FT TRANSMEM 583 603 POTENTIAL.
FT TRANSMEM 635 655 POTENTIAL.
FT TRANSMEM 658 678 POTENTIAL.
FT TRANSMEM 693 713 POTENTIAL.
FT TRANSMEM 729 749 POTENTIAL.
FT TRANSMEM 797 817 POTENTIAL.
FT TRANSMEM 840 860 POTENTIAL.
FT TRANSMEM 887 907 POTENTIAL.
FT TRANSMEM 922 942 POTENTIAL.
SQ SEQUENCE 1120 AA; 127215 MW; 809895660D2BD44 CRC64;

Query Match 11.1%; Score 78.5; DB 1; Length 1120;
Best Local Similarity 24.0%; Pred. No. 26;
Matches 24; Conservative 16; Mismatches 41; Indels 19; Gaps 2;

QY 4 TSTTFVAENRPTGETFDVMEALLRVKSSERLAMLALAGMCGHRVLPFGTASATAA 63
DB 997 TDTTTLRLVGLVAYGSDLEKVRKVLKAAATEHPRVM-----HEPMEVFFTFAGA 1047
QY 64 TVTPKASMKLPPRPQSTKSPELRELSRKIRENMKTISO 103
DB 1048 STLDHRLRYR-----ELDRSRTVDLARTIDQ 1077

RESULT 3
VATI_AERPE
ID VATI_AERPE STANDARD; PRT; 686 AA.
AC Q9YEA0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE V-type ATP synthase subunit I (EC 3.6.3.14) (V-type ATPase subunit I).
GN ATP1 OR APE0673.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankaei A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1";
RL DNA Res. 6:83-101(1999).

CC -!- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
CC GRADIENT ACROSS THE MEMBRANE.
CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
CC H(+) (Out).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF000060; BAA79646.1; --
CC PIR; F72655; F72655.
CC InterPro; IPR002490; V_ATPase_sub116.
CC Pfam; PF01496; V_ATPase_sub_1.
CC KEGG; Hydrolase; Hydrogen ion transport; Transmembrane; Complete proteome.
CC FT TRANSMEM 173 193 POTENTIAL.
CC FT TRANSMEM 349 369 POTENTIAL.
CC FT TRANSMEM 395 415 POTENTIAL.
CC FT TRANSMEM 465 485 POTENTIAL.
CC FT TRANSMEM 539 559 POTENTIAL.
CC FT TRANSMEM 605 625 POTENTIAL.
CC FT TRANSMEM 627 647 POTENTIAL.
CC SQ SEQUENCE 686 AA; 75133 MW; D90A5D479Q29D8FB CRC64;

CC Query Match 11.0%; Score 78; DB 1; Length 686;
CC Best Local Similarity 25.4%; Pred. No. 15;
CC Matches 30; Conservative 15; Mismatches 39; Indels 34; Gaps 4;

CC QY 49 GHRVLFGTASAIATVTPKASMLKPPRPOSTKSPRLRLSRKI-----REM 97
CC DB 175 GLAAVEASGGVVAVAVPKGALSKI-----SPEILRLNLSIYTPPEGVGSPREA 225
CC QY 98 NKTIQESARVNHRLPEGHPLLEKR-----AEY-----FHLRLSLKSGVNRLLI 141
CC DB 226 MEYIRGEKARGLRLVSIQEMASERLGLAEFTVVTAFENIFKFLVSLRGRTRIV 293

CC RESULT 4
CC VP5_BRD
CC ID VP5_BRD STANDARD; PRT; 480 AA.
CC AC P21230;
CC DT 01-MAY-1991 (Rel. 18, Created)
CC DT 01-MAY-1991 (Rel. 18, Last sequence update)
CC DT 15-DEC-1998 (Rel. 37, Last annotation update)
CC DE Outer capsid protein VP5.
CC GN S5.
CC OS Broadhaven virus (BRD).
CC OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
CC OX NCBI_TaxID=10893;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=91021056; PubMed=2171220;
CC RA Moss S.R., Fukusho A., Nuttall P.A.;
CC RT "RNA segment 5 of broadhaven virus, a tick-borne orbivirus, shows
CC sequence homology with segment 5 of bluetongue virus.";
CC RL Virology 179:482-484(1990).
CC CC -!- FUNCTION: THE VP5 PROTEIN IS ONE OF THE TWO PROTEINS (WITH VP2)
CC WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID.
CC CC -!- SIMILARITY: BELONGS TO THE REOVIRUSES VP5 FAMILY.
CC
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CC
CC EMBL; M58030; AAA42802.1; --
CC

DR PIR; A45339; A45339.
DR InterPro; IPR000145; Orbi_VP5.
DR Pfam; PF00901; Orbi_VP5; 1.
DR KW Coat protein.
DR SQ SEQUENCE 480 AA; 52522 MW; 28DFD78B2BE923A1 CRC64;

CC Query Match 10.9%; Score 77.5; DB 1; Length 480;
CC Best Local Similarity 24.6%; Pred. No. 12;
CC Matches 33; Conservative 22; Mismatches 60; Indels 19; Gaps 5;

CC QY 14 NRTFTETFDVMEALLRVKSSERLAMLALAGMCHRVLPGT--GASATAATVTPKGAS 71
CC DB 15 NRIGSGITRAARSDDTTKRIPSAAGRAVERVAASEIGORAIAGVVEGAATAALTGESVGES 74
CC QY 72 MK-----LXPPRPQSTKSPRLRLSRKI-----REM 122
CC DB 75 VKRAVILNVAGVHQTVPDPLNVEI-ETQAKRLDLANKREEAQIRH-----NKSMLOKE 129
CC QY 123 AEYF---RHLSLK 133
CC DB 130 AQILGEVQHLMTVQ 143

CC RESULT 5
CC VIF_HVIB1
CC ID VIF_HVIB1 STANDARD; PRT; 192 AA.
CC AC P03401;
CC DT 21-JUL-1986 (Rel. 01, Created)
CC DT 13-AUG-1987 (Rel. 05, Last sequence update)
CC DT 01-JUL-1993 (Rel. 26, Last annotation update)
CC DE Vifion infectivity factor (SOR protein).
CC GN VIF.
CC OS Human immunodeficiency virus type 1 (BH10 isolate) (HIV-1),
CC OS Human immunodeficiency virus type 1 (BRU isolate) (HIV-1),
CC OS Human immunodeficiency virus type 1 (Clone 12) (HIV-1),
CC OS Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1), and
CC OS Human immunodeficiency virus type 1 (PV22 isolate) (HIV-1).
CC OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
CC OX NCBI_TaxID=11678, 11686, 11679, 11706, 11700;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Isolate BH10;
CC RX MEDLINE=85111123; PubMed=2578615;
CC RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
CC RA Josephs S.F., Doran E.R., Rafalski J.A., Whitehorn E.A.,
CC RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
CC RA Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C.,
CC RA Wong-Staal F.;
CC RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
CC RL Nature 313:277-284(1985).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=CLONE 12;
CC RX MEDLINE=86177573; PubMed=3008154;
CC RA Arya S.K., Gallo R.C.;
CC RT "Three novel genes of human T-lymphotropic virus type III: immune
CC reactivity of their products with sera from acquired immune
CC deficiency syndrome patients.";
CC RL Proc. Natl. Acad. Sci. U.S.A. 83:2209-2213(1986).
CC RN [3]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Isolate BRU;
CC RX MEDLINE=85099333; PubMed=2981635;
CC RA Wain-Hobson S., Sonigo P., Dancs O., Cole S., Alison M.;
CC RT "Nucleotide sequence of the AIDS virus, LAV.";
CC RL Cell 40:9-17(1985).
CC RN [4]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Isolate PV22;
CC RX MEDLINE=85111157; PubMed=2982104;
CC RA Muesing M.A., Smith D.H., Cabradilla C.D., Benton C.V., Lasky L.A.,
CC RA Capon D.J.;
CC RT "Nucleic acid structure and expression of the human

RT AIDS/lymphadenopathy retrovirus.";
RL Nature 313:450-458 (1985).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Isolate HX82;
RX MEDLINE=87299196; PubMed=3040055;
RA Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Liou R.-S.,
RA Gallo R.C., Wong-Staal F.;
RT "Complete nucleotide sequences of functional clones of the AIDS
virus."
RL AIDS Res. Hum. Retroviruses 3:57-69 (1987).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
CC
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CC
CC EMBL; K02083; AAB59868.1; -
CC EMBL; M15654; AAA44202.1; -
CC EMBL; M11840; AAA44997.1; -
CC EMBL; K02013; AAB59748.1; -
CC EMBL; K01762; -; NOT ANNOTATED_CDS.
CC EMBL; K03455; AAB50230.1; -
CC EMBL; A04321; CAA00351.1; -
CC PIR; A04002; ASLJ53.
CC HIV; M11840; VIFSPCV12.
CC HIV; M15654; VIFSBH102.
CC HIV; K02013; VIFSPBRU.
CC HIV; K02083; VIFSPV22.
CC HIV; K03455; VIFSHXB2.
CC InterPro; IPR000475; Viral_infect.
CC Pfam; PF00559; Vif; 1.
CC PRINTS; PR00349; VIRIONINFECT.
CC ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22513 MW; D22589F3955CBE40 CRC64;

Query Match 10.9%; Score 77; DB 1; Length 192;
Best Local Similarity 27.9%; Pred. No. 4.2;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

Qy 22 FDVMEALLRVKSSERLAMLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157

Qy 73 KLKPPRQSTKSPRLRELSKIRENMKNTISOESARVNHRLPEGH 116
Db 158 KIKPPLPSVTKLTDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 6
VIF_HVINA
ID_VIF_HVINA STANDARD; PRT; 192 AA.
AC P31820;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Virion infectivity factor (SOR protein).
GN VIF.
OS Human immunodeficiency virus type 1 (NIT-A isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=36376;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92015467; PubMed=1920615;
RA Sakai K., Ma X., Gordienko I., Volsky D.J.;
RT "Recombinational analysis of a natural noncytopathic human
RT immunodeficiency virus type 1 (HIV-1) isolate: role of the vif gene
RT in HIV-1 infection kinetics and cytopathicity."

Qy 22 FDVMEALLRVKSSERLAMLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157

Qy 73 KLKPPRQSTKSPRLRELSKIRENMKNTISOESARVNHRLPEGH 116
Db 158 KIKPPLPSVTKLTDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 7
VIF_HVIB5
ID_VIF_HVIB5 STANDARD; PRT; 192 AA.
AC P04598;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Virion infectivity factor (SOR protein).
GN VIF.
OS Human immunodeficiency virus type 1 (BH5 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11682;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85111123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.P., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284 (1985).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
CC
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CC
CC EMBL; K02012; AAA44654.1; -
CC HIV; K02012; VIFSHS.
CC InterPro; IPR000475; Viral_infect.
CC Pfam; PF00559; Vif; 1.
CC PRINTS; PR00349; VIRIONINFECT.
CC ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22520 MW; AC17E169F5354493 CRC64;

Query Match 10.7%; Score 76; DB 1; Length 192;
Best Local Similarity 27.9%; Pred. No. 5.2;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

Qy 22 FDVMEALLRVKSSERLAMLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157

Qy 73 KLKPPRQSTKSPRLRELSKIRENMKNTISOESARVNHRLPEGH 116

RL J. Virol. 65:5765-5773 (1991).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
CC PIR; A41308; ASLJNA.
DR InterPro; IPR000475; Viral_infect.
DR Pfam; PF00559; Vif; 1.
DR PRINTS; PR00349; VIRIONINFECT.
DR ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22611 MW; 9E45529E2387DE8A CRC64;

Query Match 10.9%; Score 77; DB 1; Length 192;
Best Local Similarity 27.9%; Pred. No. 4.2;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

Qy 22 FDVMEALLRVKSSERLAMLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157

Qy 73 KLKPPRQSTKSPRLRELSKIRENMKNTISOESARVNHRLPEGH 116
Db 158 KIKPPLPSVTKLTDR-----WNKPQTKGHRGSHTM-NGH 192

RESULT 7
VIF_HVIB5
ID_VIF_HVIB5 STANDARD; PRT; 192 AA.
AC P04598;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Virion infectivity factor (SOR protein).
GN VIF.
OS Human immunodeficiency virus type 1 (BH5 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11682;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85111123; PubMed=2578615;
RA Ratner L., Haseltine W., Patarca R., Livak K.J., Starcich B.R.,
RA Josephs S.P., Doran E.R., Rafalski J.A., Whitehorn E.A.,
RA Baumeister K., Ivanoff L., Petteway S.R. Jr., Pearson M.L.,
RA Lautenberger J.A., Papas T.S., Graybe J., Chang N.T., Gallo R.C.,
RA Wong-Staal F.;
RT "Complete nucleotide sequence of the AIDS virus, HTLV-III.";
RL Nature 313:277-284 (1985).
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
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CC
CC EMBL; K02012; AAA44654.1; -
CC HIV; K02012; VIFSHS.
CC InterPro; IPR000475; Viral_infect.
CC Pfam; PF00559; Vif; 1.
CC PRINTS; PR00349; VIRIONINFECT.
CC ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22520 MW; AC17E169F5354493 CRC64;

Query Match 10.7%; Score 76; DB 1; Length 192;
Best Local Similarity 27.9%; Pred. No. 5.2;
Matches 29; Conservative 11; Mismatches 32; Indels 32; Gaps 5;

Qy 22 FDVMEALLRVKSSERLAMLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
Db 112 FDCFSDSAIR-----KALLGHIVSPRCEYQAGHNKVGSLQYLALALITPK---- 157

Qy 73 KLKPPRQSTKSPRLRELSKIRENMKNTISOESARVNHRLPEGH 116

Db 158 KVKPPLPSVTKLTEDR-----WNKPKTKGHRGSHTW-NGH 192

QY 118 LLEKRAEYFRHLRSI-----KSGQVNRLL 141

Db 121 ALELRARCSPRKLLQMDLTPEDISRLV 149

RESULT 8

DH12 RAT
ID DH12 RAT STANDARD; PRT; 400 AA.
AC P50233;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Corticosteroid 11-beta-dehydrogenase, isozyme 2 (EC 1.1.1.146) (11-
DH2) (11-beta-hydroxysteroid dehydrogenase type 2) (11-beta-HSD2)
DE (NAD-dependent 11-beta-hydroxysteroid dehydrogenase).
GN HSD11B2 OR HSD11K.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=95377198; PubMed=7643078;
RA Zhou M.-Y., Gomez-Sanchez E.F., Cox D.L., Cosby D.,
RA Gomez-Sanchez C.E.;
RT "Cloning, expression, and tissue distribution of the rat nicotinamide
adenine dinucleotide-dependent 11 beta-hydroxysteroid
dehydrogenase";
RT Endocrinology 136:3729-3734 (1995).
RL
CC -1- FUNCTION: Catalyzes the conversion of cortisol to the inactive
metabolite cortisone. Modulates intracellular glucocorticoid
levels, thus protecting the nonselective mineralocorticoid
receptor from occupation by glucocorticoids.
CC -1- CATALYTIC ACTIVITY: An 11-beta-hydroxysteroid + NAD(+) = an
11-oxosteroid + NADH.
CC -1- SUBUNIT: Interacts with ligand-free cytoplasmic NR3C2 (By
similarity).
CC -1- SUBCELLULAR LOCATION: Microsomal.
CC -1- TISSUE SPECIFICITY: Highly expressed in kidney, adrenal gland and
distal colon. Detected at much lower levels in lung.
CC -1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
(SDR) family.
CC
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CC
CC ENBL; U2424; AAA87007.1; --
DR HSP; P14061; IFDU.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NAD; Microsome.
FT NP_BIND 82 111 NAD (BY SIMILARITY).
FT ACT_SITE 232 232 BY SIMILARITY.
SQ SEQUENCE 400 AA; 43726 MW; A1BAA328E2F189D CRC64;
Query Match 10.5%; Score 74.5; DB 1; Length 400;
Best Local Similarity 25.5%; Pred. No. 17;
Matches 38; Conservative 25; Mismatches 57; Indels 29; Gaps 6;
QY 16 PTFGETDVMEALLRVKSE-----RLAMRLAGMCGHVLPGTGASAIATVT 66
Db 7 PSGAWLLVAARALLQLRSLDRIGRELLAALAAALDWJC-QLRLPPPAALVVLGAG 65
QY 67 PKGASMKLKPRL-POSTKSPSL-----RELRSKIREMKNKTSQBSARVNRHLPFGHP 117
Db 66 WIALSRLARPPRLPVATRAVLITCDTGFGKETAKKLDAMGFTVLTVDLN-----GPG 120

RESULT 9

TLPB BACSU
ID TLPB BACSU STANDARD; PRT; 662 AA.
AC P39217;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methyl-accepting chemotaxis protein tlpB.
GN TLPB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / OI1085;
RX MEDLINE=94245722; PubMed=818684;
RA Hanlon D.W., Ordal G.W.;
RT "Cloning and characterization of genes encoding methyl-accepting
chemotaxis proteins in Bacillus subtilis";
RL J. Biol. Chem. 269:14038-14046 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrati E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klier-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis";
RL Nature 390:249-256 (1997).
CC -1- FUNCTION: CHEMOTACTIC-SIGNAL TRANSDUCERS RESPOND TO CHANGES IN THE
CONCENTRATION OF ATTRACTANTS AND REPELLENTS IN THE ENVIRONMENT,
TRANSDUCE A SIGNAL FROM THE OUTSIDE TO THE INSIDE OF THE CELL, AND
FACILITATE SENSORY ADAPTATION THROUGH THE VARIATION OF THE LEVEL
OF METHYLATION. ALL AMINO ACIDS SERVE AS ATTRACTANTS IN
B.SUBTILIS, THEY APPEAR TO CAUSE AN INCREASE IN THE TURNOVER
METHYL GROUPS, LEADING TO METHYLATION OF AN UNIDENTIFIED ACCEPTOR,
WHILE REPELLENTS HAVE BEEN SHOWN TO CAUSE A DECREASE IN METHYL
GROUP TURNOVER. THE METHYL GROUPS ARE ADDED BY A METHYLTRANSFERASE
AND REMOVED BY A METHYLESTERASE.
CC -1- SIMILARITY: Contains 1 methyl-accepting transducer domain.
CC -1- SIMILARITY: Contains 1 HAMP domain.

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DR EMBL; L29189; AAA20557.1; -;
DR EMBL; Z99119; CAB15101.1; -;
DR EMBL; Z99120; CAB15112.1; -;
DR PIR; D54078; D54078.
DR HSP; P02942; 1QU7.
DR Subtilisin; BG10862; tipB.
DR InterPro; IPR004010; Cache.
DR InterPro; IPR004089; Chmtaxis_transd.
DR InterPro; IPR003660; HAMP.
DR InterPro; IPR003122; TarH.
DR Pfam; PF02743; Cache; 1.
DR Pfam; PF00672; HAMP; 1.
DR Pfam; PF00015; MCPsignal; 1.
DR Pfam; PF02203; TarH; 1.
DR SMART; SMC0304; HAMP; 1.
DR SMART; SMC0283; MA; 1.
DR SMART; SMC0319; TarH; 1.
DR PROSITE; PSS0111; CHEMOTAXIS_TRANSDUC_2; 1.
DR Chemotaxis; Transducer; Transmembrane; Methylation; Complete proteome.
KW DOMAIN 1 16
FT CYTOPLASMIC (POTENTIAL).
FT POTENTIAL.
FT TRANSMEM 17 37
FT EXTRACELLULAR (POTENTIAL).
FT DOMAIN 38 281
FT TRANSMEM 282 302
FT DOMAIN 303 662
FT DOMAIN 303 355
FT HAMP.
FT CYTOPLASMIC (POTENTIAL).
FT METHYL-ACCEPTING TRANSDUCER.
FT METHYLATION (BY SIMILARITY).
FT DEAMIDATION AND METHYLATION
FT (BY SIMILARITY).
FT METHYLATION (BY SIMILARITY).
FT MOD_RES 629 636
FT MOD_RES 636 636
FT SEQUENCE 662 AA; 71535 MW; 91215F86293D7425 CRC64;

Query Match 10.5%; Score 74; DB 1; Length 662;
Best Local Similarity 24.1%; Pred. No. 35;
Matches 27; Conservative 26; Mismatches 53; Indels 6; Gaps 3;

QY 30 LRVKSRERLMLRALAGMCHRVLPFGTASAIATVTP--KGASMKLKPFPQKTSPE- 86
DB 469 LETSKDITSLNVINGIADQTNLLALNAIEARAGEYGRGFSVAEEVRLAVQSADS 528
QY 87 LRLSRKIREMNKTIQSBSA---RVNHLPGHPLLEKRAEYFRHLRLSKSQ 135
DB 529 AKIEGLIQLIEVREISTSLSMFQSYNHEVKEGLQITDQTAEFRQIYEMTTQ 580

RESULT 10

VF2_BRD
ID_VP2_BRD STANDARD; PRT; 908 AA.
AC P35934;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Structural core protein VP2.
GN S2.
OS Broadhaven virus (BRD).
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OX NCBI_TaxID=10893;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=93019012; PubMed=1328474;
RA Moss S.R., Jones L.D., Nuttall P.A.;
RT "Comparison of the major structural core proteins of tick-borne and
RT Culicoides-borne orbiviruses."

RL J. Gen. Virol. 73:2585-2590(1992).
CC -!- SIMILARITY: BELONGS TO THE REOVIRUS VP3 FAMILY.
CC
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CC or send an email to license@isb-sib.ch).

DR EMBL; M87875; -; NOT_ANNOTATED_CDS.
DR PIR; JQ1938; JQ1938.
DR HSP; P56582; 2BVV.
DR InterPro; IPR002614; Orbi_VP3.
DR Pfam; PF01700; Orbi_VP3; 1.
DR ProDom; PD004438; Orbi_VP3; 1.
KW Core protein.
SQ SEQUENCE 908 AA; 102895 MW; 37A006EBD22CFEF7 CRC64;

Query Match 10.5%; Score 74; DB 1; Length 908;
Best Local Similarity 25.3%; Pred. No. 52;
Matches 22; Conservative 13; Mismatches 30; Indels 22; Gaps 2;

QY 73 KLKPPRPQSTKSPELR-----ELSRKIREMNKTIQSBSARVNHRLPE 114
DB 7 RVQTERQQNNSPYLRGDEVDHDPGIALSVFALQELIRKVRSTSLRNEGVEVNPAPPE 66
QY 115 GHPLLEKRAEYFRHLRLSKSQGVNRLI 141
DB 67 ----IEQIFSAHLRLDERPYRIERTL 89

RESULT 11

ID_VIOC_CHRVO STANDARD; PRT; 429 AA.
AC Q9S3U9; Q9S0N3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DT Probable monooxygenase vIOC (EC 1.-.-.-).
GN VIOC.
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=UQM51;
RX MEDLINE=20525185; PubMed=11075927;
RA August P.R., Grossman T.H., Minor C., Draper M.P., MacNeil I.A.,
RA Pemberton J.M., Call K.M., Holt D., Osburne M.S.;
RT "Sequence analysis and functional characterization of the violacein
RT biosynthetic pathway from Chromobacterium violaceum.";
RL J. Mol. Microbiol. Biotechnol. 2:513-519(2000).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=JCM 1249;
RA Hoshino T.;
RT "Biosynthetic gene cluster for violacein pigment.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: Prodeoxyviolacein + O(2) = deoxyviolacein.
CC -!- COFACTOR: FAD (Potential).
CC -!- PATHWAY: Violacein biosynthesis; common branch; second step.
CC -!- INDUCTION: By N-acetylhomoserine lactone (AHL).
CC -!- BIOTECHNOLOGY: Violacein production is used as a biosensor for the
CC detection of quorum-sensing AHL production. Violacein possesses
CC antibacterial, antiviral, antimicrobial, antileishmanial,
CC trypanocidal and potential antitumoral activities.
CC
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DR EMBL; AF172851; AAD51810.1; -
DR EMBL; AB033299; BAA84784.1; -
DR InterPro; IPR000733; Flav_monooxygenase.
DR Pfam; PF01360; Monooxygenase; 1.
KW Oxidoreductase; Monooxygenase; Flavoprotein; FAD;
KW Antibiotic biosynthesis.
FT NP_BIND 3 21 FAD (POTENTIAL).
FT CONFLICT 38 38 Q -> R (IN REF. 2).
SQ SEQUENCE 429 AA; 47948 MW; ALD1966CA9739895 CRC64;
Query Match 10.4%; Score 73.5; DB 1; Length 429;
Best Local Similarity 25.3%; Pred. No. 23;
Matches 41; Conservative 16; Mismatches 54; Indels 51; Gaps 8;
QY 3 STSTTNFVAENRPTGCTFD-----VMREALLR--VKSSERLAMLRA----- 43
DB 245 SPSLTTT-----DEPTWRAFDYFGGLPRDADEMLRQFLAKPSNDLINVRSSTHYKGN 300
QY 44 --LAGMCGHRVLPGTGASIAATVTPKGSMKLPKR-----PQSTKSPELREL 90
DB 301 VLLLGDAAHATAPFLG-----QGMMALEDARTVELLDRHQGDQKAFPEFTTEL 350
QY 91 SRKIREMNKTSQESARVNHRLPEGHPLLEKRAEYFRHLRS 131
DB 351 ----RKVQADAMQDMARANYDLVLSNPIFFWRARYTRYMHS 388
RESULT 12
YGY3 HALSQ STANDARD; PRT; 437 AA.
AC P21561;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical 50.6 kDa protein in the 5' region of gyra and gyvB (ORF 3).
DE Haloferax sp. (strain Aa 2.2).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Haloferax.
OX NCBI_TaxID=2254;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91100352; PubMed=1846146;
RA Holmes M.L., Dyall-Smith M.L.;
RT "Mutations in DNA gyrase result in novobiocin resistance in halophilic archaeobacteria".
RL J. Bacteriol. 173:642-648 (1991).
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KW Hypothetical protein.
SQ SEQUENCE 437 AA; 50626 MW; B5B99A2AF3892BEF CRC64;
Query Match 10.4%; Score 73.5; DB 1; Length 437;
Best Local Similarity 29.5%; Pred. No. 24;
Matches 31; Conservative 9; Mismatches 44; Indels 21; Gaps 5;
QY 19 GETFDVREALLRVKSSERLAMLRLAGMCGHR-VLPGTGASIAATVTPKGSMKLPK-- 75
DB 269 GEARGLPERPPLGVRTVHGGRIGRVGAGRPQVPGDFA-----PQGEDSERRET 320

QY 76 PPRQSTKSPELRELRSKIREMNKTSQESARVNHRLPEGHPL 117
DB 321 PPRPHSRKRRTGTGAHHRHRRRR-----RVHREGALPAHP 358
RESULT 13
PTNE HUMAN STANDARD; PRT; 1187 AA.
AC Q15678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase pez).
GN PTFN14 OR PEZ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95251727; PubMed=7733990;
RA Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V., Crompton M.R.;
RT "Pez: a novel human cDNA encoding protein tyrosine phosphatase- and ezrin-like domains".
RL Biochem. Biophys. Res. Commun. 209:959-965 (1995).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein tyrosine + phosphate.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF HUMAN TISSUES INCLUDING KIDNEY, SKELETAL MUSCLE, LUNG AND PLACENTA.
CC -!- SIMILARITY: Contains 1 FERM domain.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-TYROSINE PHOSPHATASE FAMILY.
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DR PIR; JC4155; JC4155.
DR HSSP; P29350; 1GWZ.
DR Genew; HGNC:9647; PTFN14.
DR MIM; 603155;
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR000387; TYR_Phosphatase.
DR InterPro; IPR000242; Tyr_Pp.
DR Pfam; PF00373; Band 4.1; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND4.1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00660; FERM_1; 1.
DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS0057; FERM_3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR Structural protein; Cytoskeleton; Hydrolase.
FT DOMAIN 21 306 FERM.
FT DOMAIN 933 1187 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1121 1121 BY SIMILARITY.
FT DOMAIN 566 576 POLY-PRO.
FT DOMAIN 709 716 POLY-GLU.
SQ SEQUENCE 1187 AA; 135239 MW; 015760B75E3574E3 CRC64;

Query Match 10.4%; Score 73.5; DB 1; Length 1187;
 Best Local Similarity 27.3%; Pred. No. 79;
 Matches 27; Conservative 19; Mismatches 16; Indels 37; Gaps 5;

QY 50 HRVLPFG-TGASAIATV-TPKGASKLK-----PPRPO-----STKSP 85
 DB 521 NNVPSKPGASAIHTVSTPLANKQLOSHNYSTAHMLKNYLFRRPPPPRPPRAITSP 580
 QY 86 ELRE-----LSRKIRENMKTIQSARVNH 111
 DB 581 DLASHRRHYVSGSPDLVTRKVLQSVKTFQDSSPVVHQ 619

RESULT 14
 VIF_HV1SC STANDARD; PRT; 109 AA.
 AC P05899;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Viron infectivity factor (SOR protein) (Fragment).
 GN VIF.
 OS Human immunodeficiency virus type 1 (SC isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11702;
 RN [1]
 RP MEDLINE=88219542; PubMed=3369091;
 RA Gurgu C., Guo H.-G., Franchini G., Aldovini A., Collalti E.,
 RA Farrell K., Wong-Staal F., Gallo R.C., Reitz M.S. Jr.;
 RT "Envelope sequences of two new United States HIV-1 isolates.";
 RL Virology 164:531-536(1988).
 CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
 CC -!- MISCELLANEOUS: THE SC ISOLATE WAS TAKEN FROM AN ARC PATIENT IN
 CC 1984 IN SOUTHERN CALIFORNIA.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M17450; AAA45059.1; -
 DR HIV; M17450; VIFSCC.
 DR InterPro; IPR000475; Viral_infect.
 DR Pfam; PF00559; Vif; 1.
 DR PRINTS; PRO0349; VIRIONINFECT.
 DR ProDom; PD000063; Viral_infect; 1.
 KW AIDS.
 FT NON_TER
 FT SEQUENCE 109 AA; 12308 MW; 3D1BB3599F78B727 CRC64;

Query Match 10.3%; Score 73; DB 1; Length 109;
 Best Local Similarity 32.0%; Pred. No. 4.9;
 Matches 32; Conservative 9; Mismatches 35; Indels 24; Gaps 6;

QY 22 FDMVEALLRVKSSERLAMLAL-AGWC-----GHRVLPGTGASAIATVTPKGASKLK 76
 DB 29 FDCFS-----SAIRNAILGALVSGKCEYQAGHNKVGSLQYLALTALITFK-----KTRP 78
 QY 77 PRPOSTKSPELRSRKIRENMKTIQSARVNHRLPEGH 116
 DB 79 PLPSVRKLTEDR-----WNKPQKTGHRGSHMTM-NGH 109

RESULT 15
 FLID_VIBCH STANDARD; PRT; 666 AA.
 AC Q9XQ63;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Flagellar hook-associated protein 2 (HAP2) (Filament cap protein)
 DE (Flagellar cap protein).
 GN FLID OR VC2140.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae.";
 RL Nature 406:477-483(2000).
 CC -!- FUNCTION: REQUIRED FOR THE MORPHOGENESIS AND FOR THE ELONGATION OF
 CC THE FLAGELLAR FILAMENT BY FACILITATING POLYMERIZATION OF THE
 CC FLAGELLIN MONOMERS AT THE TIP OF GROWING FILAMENT. FORMS A CAPPING
 CC STRUCTURE, WHICH PREVENTS FLAGELLIN SUBUNIT (TRANSPORTED THROUGH
 CC THE CENTRAL CHANNEL OF THE FLAGELLUM) FROM LEAKING OUT WITHOUT
 CC POLYMERIZATION AT THE DISTAL END (BY SIMILARITY).
 CC -!- SUBUNIT: Homopentamer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Flagellar.
 CC -!- SIMILARITY: BELONGS TO THE FLID FAMILY.
 CC -----
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 CC -----
 CC EMBL; A3004287; R8F95285.1; -
 DR PIR; G82111; G82111.
 DR TIGR; VC2140; -
 DR InterPro; IPR003481; FLID.
 DR Pfam; PF02465; FLID; 1.
 KW Flagella; Coiled coil; Complete proteome.
 FT DOMAIN 354 419 COILED COIL (POTENTIAL).
 FT SEQUENCE 666 AA; 72330 MW; 6794EFEC34A2A0D2 CRC64;

Query Match 10.3%; Score 73; DB 1; Length 666;
 Best Local Similarity 25.4%; Pred. No. 44;
 Matches 31; Conservative 21; Mismatches 52; Indels 16; Gaps 4;

QY 30 LRVKSSERLAMLALAGMCGHRVLPGTGASAI-----AATVTPKGASKLK-----K 75
 DB 136 LDVQGNKSLVDI--VRGNGEKSNFGVRASINDVEGRLIVASVNGKDHVKMSAQAE 193
 QY 76 PRPOSTKSPELRSRKIRENMKTIQSARVNHRLPEGHPLLEKRAPIYFPHLSLSKQ 135
 DB 194 PGNP--LKOLEYKTLQVRVRLDEKARAQAQLIAPLTPEQQKVAAKVAEKIGDAARLVQD 251
 QY 136 GV 137
 DB 252 EV 253

RESULT 16
 PHSA_STRAT STANDARD; PRT; 642 AA.
 ID PHSA_STRAT
 AC Q53692;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

Phenoxazinone synthase (EC 1.1.1.11) (PHS).

PhSA.

GN Streptomyces antibioticus.

OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomyces; Streptomycetaceae; Streptomyces.

OC NCBI_TaxID=1890;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-15.

RC STRAIN=IMRU 3720; PubMed=7592317;

RX MEDLINE=96011355; PubMed=7592317;

RA Hsieh C.-J., Jones G.H.;

RT "Nucleotide sequence, transcriptional analysis, and glucose regulation of the phenoxazinone synthase gene (phsA) from Streptomyces antibioticus."

RT J. Bacteriol. 177:5740-5747 (1995).

RL [2]

RN SUBUNITS.

RP MEDLINE=82066838; PubMed=7305384;

RX Choy H.A., Jones G.H.;

RT "Phenoxazinone synthase from Streptomyces antibioticus: purification of the large and small enzyme forms."

RT Arch. Biochem. Biophys. 211:55-65 (1981).

RL -1- FUNCTION: CATALYZES THE LAST BUT TWO STEPS IN THE PUTATIVE BIOSYNTHETIC PATHWAY OF ACTINOMYCIN.

CC -1- CATALYTIC ACTIVITY: 4 4-methyl-3-hydroxyanthraniloyl pentapeptide + 3 O(2) = 2 actinomycin acid + 6 H(2)O.

CC -1- COFACTOR: THIS PROTEIN BELONGS TO THE MULTICOPPER OXIDASES WHICH CONTAIN THREE DISTINCT CU CENTERS KNOWN AS TYPE 1 OR BLUE, TYPE 2 OR NORMAL, AND TYPE 3 OR COUPLED BINUCLEAR (BY SIMILARITY).

CC -1- SUBUNIT: HOMODIMER (SMALL FORM) OR HOMOHETEROMER (LARGE FORM).

CC -1- SIMILARITY: BELONGS TO THE FAMILY OF MULTICOPPER OXIDASES.

CC -1- SIMILARITY: Contains 2 plastocyanin-like domains.

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CC EMBL; U04283; AAA86668.1; ALT_INIT.

CC HSSP; P36649; 1KV7.

DR InterPro; IPR001117; Cu-oxidase.

DR InterPro; IPR002355; MultiCu_oxidase2.

DR Pfam; PF00394; Cu-oxidase; 1.

DR PROSITE; PS00079; MULTICOPPER_OXIDASE1; 1.

DR PROSITE; PS00080; MULTICOPPER_OXIDASE2; 1.

KW Oxidoreductase; Repeat; Metal-binding; Copper;

KW Antibiotic biosynthesis.

FT INIT MET 0

FT DOMAIN 86 223 PLASTOCYANIN-LIKE 1.

FT METAL 433 620 PLASTOCYANIN-LIKE 2.

FT COPPER (TYPE 2) (BY SIMILARITY).

FT METAL 161 161 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 163 163 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 201 201 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 203 203 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 524 524 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 527 527 COPPER (TYPE 2) (BY SIMILARITY).

FT METAL 529 529 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 602 602 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 603 603 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 604 604 COPPER (TYPE 3) (BY SIMILARITY).

FT METAL 608 608 COPPER (TYPE 1) (BY SIMILARITY).

FT METAL 613 613 COPPER (TYPE 1) (BY SIMILARITY).

SEQUENCE 642 AA; 70113 MW; E0B39C0BA3364E48 CRC64;

Query Match 10.2%; Score 72; DB 1; Length 642;

Best Local Similarity 25.6%; Pred. No. 52;

Matches 30; Conservative 17; Mismatches 40; Indels 30; Gaps 6;

15 RPT---FGETEDVMEALLRVKSSRLAMRLAGMCGHRV-LFGTGASAIATVTPKGA 70

345 RPVPVDFDPTLPVLSAA-----PAERFDLLVDFRALGGRRLLRVKGPAGAGTDPDPLG- 399

71 SMKLKPRPQSTKSPRELRSKRIR-----MNKTISQESARVNHRLPEGHPL 119

399 -----GVRYPEVMEF--RVRETCEDSFALPEVLGSGFRMSHDPHGRLI 443

RESULT 17

HMW2 MYCGE

ID HMW2 MYCGE STANDARD; PRT; 1805 AA.

AC P47450;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Cytochrome high molecular weight protein 2 (Cytochrome accessory protein 2).

DE HMW2 OR MG218.

GN Mycoplasma genitalium.

OS Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

OX NCBI_TaxID=2097;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33530 / G-37;

RX MEDLINE=96026346; PubMed=7569993;

RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Uterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

RA "The minimal gene complement of Mycoplasma genitalium."

RT Science 270:397-403 (1995).

RL [2]

RN SEQUENCE OF 557-659 FROM N.A.

RP STRAIN=ATCC 33530 / G-37;

RX MEDLINE=94075230; PubMed=8253680;

RA Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;

RT "A survey of the Mycoplasma genitalium genome by using random sequencing."

RT J. Bacteriol. 175:7918-7930 (1993).

CC -1- FUNCTION: COMPONENT OF THE CYTOSKELETON-LIKE STRUCTURE WHICH STABILIZES THE SHAPE OF THE WALL-LESS MYCOPLASMA. THIS CYTOSKELETON-LIKE NETWORK OF ACCESSORY PROTEINS CONTAINING HMW PROTEINS 1 TO 5 ALLOWS THE PROPER ANCHORING OF CYTADHESIN PROTEINS IN THE MYCOPLASMA MEMBRANE AT THE ATTACHMENT ORGANELLE (BY SIMILARITY).

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CC EMBL; U39701; AAC71437.1; -

CC EMBL; U02185; AAD12447.1; -

CC PIR; A64224; A64224.

CC TIGR; MG218; -

CC Pfam; PF02403; Seryl_tRNA_N; 1.

KW Cytoadherence; Structural protein; Coiled coil; Complete proteome.

FT DOMAIN 28 838 COILED COIL (POTENTIAL).

FT DOMAIN 914 1531 COILED COIL (POTENTIAL).

FT DOMAIN 1632 1723 COILED COIL (POTENTIAL).

FT DOMAIN 1777 1804 COILED COIL (POTENTIAL).

SEQUENCE 1805 AA; 216252 MW; I1D093AF173284FD CRC64;

Query Match 10.2%; Score 72; DB 1; Length 1805;

Best Local Similarity 33.3%; Pred. No. 1.8e+02;

Matches 19; Conservative 12; Mismatches 22; Indels 4; Gaps 1;

81 STKSPDEL-----RELGRKTRNMNKTISQESARVNHRLPEGHPLPEKGRVFFHRLSLK 133

RESULT 18

GIANT HUMAN STANDARD; PRT; 3259 AA.
 AC Q14789; Q14398;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Golgi autoantigen, golgin subfamily B member 1 (Giantin) (Macrogolgin)
 DE (Golgi complex-associated protein, 372-kDa) (GCP372).
 GS GOLGB1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94187728; PubMed=7511208;
 RA Seelig H.P., Schranz P., Schroeter H., Wiemann C., Griffiths G.,
 RA Renz M.
 RT "Molecular genetic analyses of a 376-kilodalton Golgi complex membrane
 RT protein (Giantin).";
 RL Mol. Cell. Biol. 14:2564-2576(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94257116; PubMed=8198703;
 RA Seelig H.P., Schranz P., Schroeter H., Wiemann C., Griffiths G.,
 RA Renz M.
 RT "Macrogolgin -- a new 376 kD Golgi complex outer membrane protein as
 RT target of antibodies in patients with rheumatic diseases and HIV
 RT infections.";
 RL J. Autoimmun. 7:67-91(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95100974; PubMed=7802676;
 RA Solda M., Misumi Y., Fujiwara T., Nishioka M., Ikehara Y.;
 RT "Molecular cloning and sequence analysis of a human 372-kDa protein
 RT localized in the Golgi complex.";
 RL Biochem. Biophys. Res. Commun. 205:1399-1408(1994).
 CC -!- FUNCTION: May participate in forming intercisternal cross-bridges
 CC of the Golgi complex.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Membrane-associated protein. Golgi.
 CC -!- DISEASE: Antigen in chronic rheumatoid arthritis and in the
 CC autoimmune disease Sjogren's syndrome.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; X75304; CAA53052.1; -;
 CC EMBL; D25542; BAA05025.1; -;
 CC PIR; A56539; A56539.
 CC PIR; I52300; I52300.
 CC Genew; HGNC:4429; GOLGB1.
 CC MIM; 602500; -;
 CC GO; GO:0000139; C:Golgi membrane; TAS.
 CC GO; GO:0005795; C:Golgi stack; TAS.
 CC GO; GO:0016021; C:integral to membrane; TAS.
 CC GO; GO:0007030; P:Golgi organization and biogenesis; TAS.
 CC GO; GO:0007030; P:Golgi stack; Antigen; Coiled coil; Transmembrane
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FT METAL 113 113 SUBUNIT.
FT METAL 116 116 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 119 119 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 123 123 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 152 152 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 155 155 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 158 158 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 162 162 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 212 AA; 23896 MW; 4D5F95E4C918FE8 CRC64;
Query Match 10.1%; Score 71.5; DB 1; Length 212;
Best Local Similarity 30.9%; Pred. No. 15;
Matches 29; Conservative 19; Mismatches 35; Indels 11; Gaps 5;
QY 39 AMLRALAGMCHRVLPVGTGASAIAT--VTPKGASMKLPPRQSTKSPKPELRELSKIR 95
DB 12 ALAQARAGACHASVGLHSSAVATKYVNLRFPSMDKSVTDRAQTLLWTEL---IR 68
QY 96 ENKTTIS---QESARVNRHRLPEGHPLLEK-RAEY 125
DB 69 GLGMLTSLVLFREPATINYPFEKG-PLSPRFRGEH 101
RESULT 20
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ID PGK_NEIMA STANDARD; PRT; 392 AA.
AC Q9JWS8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphoglycerate kinase (EC 2.7.2.3).
GN PGK OR NMA0257.
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagers K., Leather S., Moule S., Mungall K., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491.";
RL Nature 404:502-506(2000).
CC -!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-
phospho-D-glyceroyl phosphate.
CC -!- PATHWAY: Second phase of glycolysis; second step.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the phosphoglycerate kinase family.
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CC -----
CC EMBL; AL162752; CAB83565.1; -
CC PIR; E82020; E82020.
CC HSSP; P18912; 1PHP.
CC HAWAP; MF_00145; 1.
CC InterPro; IPR001576; PGK.
CC Pfam; PF0162; PGK; 1.
CC PRINTS; PRO0477; PGKLYCKINASE.
CC PROSITE; PS00111; PGKLYCERATE_KINASE; 1.

KW Transferase; Kinase; Glycolysis; Complete proteome.
SQ SEQUENCE 392 AA; 40661 MW; F6AB86C6C7BFED35 CRC64;
Query Match 10.1%; Score 71.5; DB 1; Length 392;
Best Local Similarity 25.0%; Pred. No. 32;
Matches 37; Conservative 17; Mismatches 53; Indels 41; Gaps 7;
QY 13 ENRPTGETFDVNRALLRVKSSER---LAMLRALAGMC-----CHRVLPVGTGAS 59
DB 97 ENKPAL-NAGDVMVLQNVINKGEKNDLELKGAYASLQVDFVNDAFGTAHRAQASTEAV 155
QY 60 AIAATVTPKGASMK-----LKPPRPQ-----STKSPKPELRELSKIREM--- 97
DB 156 AQAAPVACAGVLMAGELDALGKALKQAPRPMVAIVAGSKVSTKLTILESADKVDQVLI 215
QY 98 ---NKTISQESARVNRHRLPEGHPLLEK 121
DB 216 GGIANTFLLAEGKAIGKSLAE-HDLVEE 242
RESULT 21
PGK_NEIMB
ID PGK_NEIMB STANDARD; PRT; 392 AA.
AC Q9K1R0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphoglycerate kinase (EC 2.7.2.3).
GN PGK OR NMB0010.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Clecho A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58.";
RL Science 287:1809-1815(2000).
RN [2]
RP CONCEPTUAL TRANSLATION.
RA Bairoch A.;
RL Unpublished observations (OCT-2002).
CC -!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-
phospho-D-glyceroyl phosphate.
CC -!- PATHWAY: Second phase of glycolysis; second step.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -!- SIMILARITY: Belongs to the phosphoglycerate kinase family.
CC -!- CAUTION: This is a conceptual translation: a probable incorrect
CC perfect sequence repeat was excised.
CC -----
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CC -----
CC EMBL; AE002359; AAF40489.1; -
CC PIR; H81247; H81247.
CC HSSP; P18912; 1PHP.
CC TIGR; NMB0010; -.

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; 273101; CAA97383.1; ALT INIT.
CC DR EMBL; AE006977; AAK45141.1; -.
CC DR TIGR; MT0899; -.
CC DR Tuberculin; Rv0876c; -.
CC KW Hypothetical protein; Transmembrane; Complete proteome.
CC FT TRANSMEM 128 148 POTENTIAL.
CC FT TRANSMEM 155 175 POTENTIAL.
CC FT TRANSMEM 186 206 POTENTIAL.
CC FT TRANSMEM 208 228 POTENTIAL.
CC FT TRANSMEM 259 279 POTENTIAL.
CC FT TRANSMEM 283 303 POTENTIAL.
CC FT TRANSMEM 358 378 POTENTIAL.
CC FT TRANSMEM 387 407 POTENTIAL.
CC FT TRANSMEM 428 448 POTENTIAL.
CC FT TRANSMEM 490 510 POTENTIAL.
CC FT TRANSMEM 515 535 POTENTIAL.
CC SQ SEQUENCE 559 AA; 59144 MW; 0811EB61C77C5616 CRC64;

Query Match      10.1%; Score 71.5; DB 1; Length 559;
Best Local Similarity 26.6%; Pred. No. 49;
Matches 33; Conservative 16; Mismatches 34; Indels 41; Gaps 7;

QY      18 FGCTEDVNVREA-----LLBVKSSERLAMLRALAG-----MCHRV- 52
DB      228 FKSFSVLRSVAVTPRMPTDIDLVRNS--RTVFGLGGTTAGGAIAAGVEFVCTHLFQ 285
QY      53 LFGTGASAIATVTPKGASMKLKPPRPOSTKSPFLRELRSRKIRENMKTIS--QESARVNH 110
DB      286 LP--GALFWVAITTAGASLSMRIPRWEVTS-----GEVPATLSYHRDRGRRLRR 333
QY      111 RLPE 114
DB      334 RWPE 337

RESULT 23
YMW8 YEAST
ID ID YMW8 YEAST STANDARD; PRT; 732 AA.
AC AC Q03254;
DT DT 01-NOV-1997 (Rel. 35, Created)
DE DE 01-NOV-1997 (Rel. 35, Last sequence update)
DE DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE DE Hypothetical 83.4 kDa protein in DSK2-CAT8 intergenic region.
OS OS YMR277W OR YMC021.03.
OS Saccharomyces cerevisiae (Baker's yeast).
OC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX OX NCBI_TaxId=4932;
RN RN [1]
RP RP SEQUENCE FROM N.A.
RC RC STRAIN=S288c / AB972;
RX RX PubMed=9169872;
RA RA Bowman S., Churcher C.M., Badcock K., Brown D., Chillingworth T.,
RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagals K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;
RA "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT RT XIII."
RL RL Nature 387:90-93(1997).
CC CC -!- SIMILARITY: Contains 1 BRCT domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; 249704; CAA89775.1; -.

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DR PIR: S54584; S54584.
DR SGD: S0004890; FCPI.
DR GO: GO:0005634; C:nucleus; IPI.
DR GO: GO:0004721; P:protein phosphatase activity; IDA.
DR GO: GO:0006470; P:protein amino acid dephosphorylation; IDA.
DR GO: GO:0006350; P:transcription; IMP.
DR InterPro: IPR001357; BRCT.
DR InterPro: IPR004274; NIF.
DR Pfam: PF00533; BRCT; 1.
DR Pfam: PF02031; NIF; 1.
DR SMART: SM00292; BRCT; 1.
DR SMART: SM00577; CPDC; 1.
DR PROSITE: PS0172; BRCT; 1.
KW Hypothetical protein.
FT DOMAIN 499 593
SQ SEQUENCE 732 AA; 83441 MW; EACA2A7D33A983C6 CRC64;

Query Match 10.18; Score 71.5; DB 1; Length 732;
Best Local Similarity 28.18; Pred. No. 67;
Matches 27; Conservative 19; Mismatches 37; Indels 13; Gaps 4;

Qy 57 GASAIAATVTPKGSAMKLPKRPSTKSPKELREL-----SRKIRE-MNKTISQESARV 108
Db 347 GVGDINSFLPKQSTGMVLGRKTRQKSQSQELLTDIMDNKKLQEKIDKEVKRQEEKL 406

Qy 109 NHRL--PEGHPLEKRAEYFRHLR---SLKSQGVNR 139
Db 407 NHQLATAEPPANESKELTKLEYSASLEVOQNR 442

RESULT 24
CLAT_HUMAN STANDARD; PRT; 748 AA.
AC P28329; Q16488; Q9BQ23; Q9BQ35; Q9BQEL;
DT 01-DEC-1992 (Rel. 24, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Choline O-acetyltransferase (EC 2.3.1.6) (CHOA2ase) (Choline
DE acetylase) (CHAT).
GN CHAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=93180642; PubMed=1337937;
RA Oda Y., Nakanishi I., Deguchi T.;
RT "A complementary DNA for human choline acetyltransferase induces two
RT forms of enzyme with different molecular weights in cultured cells.";
RL Brain Res. Mol. Brain Res. 16:287-294(1992).
RN [2]
RP SEQUENCE FROM N.A. ALTERNATIVE SPLICING, VARIANTS FIMG2 PRO-210;
RP ALA-211; THR-305; CVS-420; LYS-441; GLY-482; LEU-498; LEU-506 AND
RP HIS-560, AND VARIANTS THR-120 AND GUY-392.
RX MEDLINE=2117155; PubMed=11172068;
RA Ohno K., Tsujino A., Brengman J.M., Harper C.M., Bajzer Z., Udd B.,
RA Beyring R., Robb S., Kirkham P.J., Engel A.G.;
RT "Choline acetyltransferase mutations cause myasthenic syndrome
RT associated with episodic apnea in humans.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:2017-2022(2001).
RN [3]
RP SEQUENCE OF 111-669 FROM N.A.
RX MEDLINE=93000480; PubMed=1388731;
RA Lorenzi M.V., Trinidad A.C., Zhang R., Strauss W.L.;
RT "Two mRNAs are transcribed from the human gene for choline
RT acetyltransferase.";
RL DNA Cell Biol. 11:593-603(1992).
RN [4]
RP SEQUENCE OF 109-232 FROM N.A.
RX MEDLINE=92155737; PubMed=1339386;
RA Toussaint J.L., Geoffroy V., Schmitt M., Werner A., Garnier J.M.,

RA PIR: S54584; S54584.
RT "Human choline acetyltransferase (CHAT) : partial gene sequence and
RT potential control regions.";
RL Genomics 12:412-416(1992).
RN [5]
RP SEQUENCE OF 688-738 FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=92149876; PubMed=1784419;
RA Cervini R., Rocchi M., DiDonato S., Finocchiaro G.;
RT "Isolation and sub-chromosomal localization of a DNA fragment of the
RT human choline acetyltransferase gene.";
RL Neurosci. Lett. 132:191-194(1991).
CC -!- FUNCTION: Catalyzes the reversible synthesis of acetylcholine
CC (ACH) from acetyl CoA and choline at cholinergic synapses.
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + choline = CoA + O-acetylcholine.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=M; Synonyms=83 kDa;
CC IsoId=P28329-1; Sequence=Displayed;
CC Name=S; Synonyms=74 kDa;
CC IsoId=P28329-2; Sequence=VSP_000790;
CC Name=R; Synonyms=70 kDa;
CC IsoId=P28329-3; Sequence=VSP_000791;
CC -!- DISEASE: Defects in CHAT are the cause of familial infantile
CC myasthenia gravis 2 (FIMG2) [MIM:254210]; also known as CMS-EA.
CC FIMG2 patients have myasthenic symptoms since birth or early
CC infancy, negative tests for anti-AChR antibodies, and abrupt
CC episodic crises with increased weakness, bulbar paralysis, and
CC apnea precipitated by undue exertion, fever, or excitement.
CC Inheritance is autosomal recessive.
CC -!- SIMILARITY: BELONGS TO THE CARNITINE/CHOLINE ACETYLTRANSFERASE
CC FAMILY.
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EMBL; S56138; AAA14245.1; -
DR EMBL; AF305907; AAK08953.1; -
DR EMBL; AF305906; AAK08950.1; -
DR EMBL; AF305894; AAK08950.1; JOINED.
DR EMBL; AF305895; AAK08950.1; JOINED.
DR EMBL; AF305896; AAK08950.1; JOINED.
DR EMBL; AF305897; AAK08950.1; JOINED.
DR EMBL; AF305898; AAK08950.1; JOINED.
DR EMBL; AF305899; AAK08950.1; JOINED.
DR EMBL; AF305900; AAK08950.1; JOINED.
DR EMBL; AF305901; AAK08950.1; JOINED.
DR EMBL; AF305902; AAK08950.1; JOINED.
DR EMBL; AF305903; AAK08950.1; JOINED.
DR EMBL; AF305904; AAK08950.1; JOINED.
DR EMBL; AF305905; AAK08950.1; JOINED.
DR EMBL; AF305908; AAK08954.1; -
DR EMBL; AF305906; AAK08951.1; -
DR EMBL; AF305894; AAK08951.1; JOINED.
DR EMBL; AF305895; AAK08951.1; JOINED.
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DR EMBL; AF305909; AAK08955.1; -
DR EMBL; AF305906; AAK08952.1; -
DR EMBL; AF305894; AAK08952.1; JOINED.

Db

QY 108 VNHRLPEGHPLLEKRAEYFRHLRLSKSQ 135
Db 131 L-FKLPV-PPLOQTATYLQCMRHVSE 156

RESULT 25

SPQC_HUMAN STANDARD: PRT: 2564 AA.
AC Q9H254; Q9H1K7, Q9H1K8; Q9H3G8; Q9HCD0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Spectrin beta chain, brain 3 (Spectrin, non-erythroid beta chain 3)
DE (Beta-IV spectrin).
GN SPTBN4 OR SPTBN3 OR KIAA1642.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21316449; PubMed=11294830;
RA Tee W.T., Tang J., Jin O., Korsgren C., John K.M., Kung A.L.,
Gwynn B., Peters L.L., Lux S.E.,
RT "A new Spectrin, beta-IV, has a major truncated isoform that
RT associates with promyelocytic leukemia protein nuclear bodies and the
RT nuclear matrix."
RL J. Biol. Chem. 276:23974-23985(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).
RX MEDLINE=20539976; PubMed=11086001;
RA Berghs S., Aggujaro D., Dirxx R. Jr., Maksimova E., Stabach P.,
Hermel J.-M., Zhang J.-P., Philbrick W., Slepnev V., Ort T.,
RA Solimena M.;
RT "BetaIV spectrin, a new spectrin localized at axon initial segments
RT and nodes of ranvier in the central and peripheral nervous system."
RL J. Cell Biol. 151:985-1002(2000).
RN [3]
RP SEQUENCE OF 386-2382 FROM N.A. (ISOFORM 1).
RX MEDLINE=20450683; PubMed=10997877;
RA Nagase T., Kikuno R., Nakayama M., Hirose M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes.
RT XVIII. The complete sequences of 100 new cDNA clones from brain which
RT code for large proteins in vitro."
RL DNA Res. 7:273-281(2000).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=1;
CC IsoId=Q9H254-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9H254-2; Sequence=VSP_000725, VSP_000726;
CC Name=3;
CC IsoId=Q9H254-3; Sequence=VSP_000723, VSP_000724;
CC Name=4;
CC IsoId=Q9H254-4; Sequence=VSP_000727, VSP_000728;
CC -!- TISSUE SPECIFICITY: Abundantly expressed in brain and pancreatic
CC islets.
CC -!- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
CC -!- SIMILARITY: Contains 2 calponin-homology (CH) domains.
CC -!- SIMILARITY: Contains 1 PH domain.
CC -!- SIMILARITY: Contains 18 spectrin repeats.
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EMBL; AF305896; AAK08952.1; JOINED.
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EMBL; AF305990; AAK08952.1; JOINED.
EMBL; AF305991; AAK08952.1; JOINED.
EMBL; AF305992; AAK08952.1; JOINED.
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Cytoskeleton; Membrane; Repeat; Actin-binding; Capping protein; Alternative splicing.
DOMAIN 1 282
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FT DOMAIN 180 282 CH 1.
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FT /FTId=VSP_000727.
FT Missing (in isoform 4).
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FT VARSPLIC 2155 2564
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FT CONFLICT 604 608 MISSING (IN REF. 2).
FT CONFLICT 714 714 L -> S (IN REF. 2).
FT CONFLICT 1189 1189 E -> K (IN REF. 2).
FT CONFLICT 1193 1193 E -> K (IN REF. 2).
FT CONFLICT 1331 1331 G -> S (IN REF. 1).
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DB 2170 AEVTRVG----IVRQLKPERLPDRIDLPETIGRVEPALPAEDAAETPATP--AA 2223
OY 72 MLKPPRPQSTKQPE-LRELSKIR-EMNKTISQESARVNHRLPE-----GHPLLE 120
DB 2224 AEQVPRPPEQESADRAELPRRRRPERQESVQSEAAARRRPERQESAHEAAHSLT 2283
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DE Virion infectivity factor (SOR protein).
GN VIF.
OS Human immunodeficiency virus type 1 (RP/HAT isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11701;
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RA Wolf H., Parks E.S., Parks W.P., Josephs S.F., Gallo R.C.,
RA Wong-Staal F.;
RL Submitted (XXX-1987) to the HIV data bank.
CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
CC
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CC HIV; M17451; VIFSRP.
CC InterPro; IPR000475; Viral_infect.
CC Pfam; PF00559; Vif; 1.
CC PRINTS; PR00349; VIRIONINFCT.
CC ProDom; PD000063; Viral_infect; 1.
CC AIDS.
SQ SEQUENCE 192 AA; 22687 MW; F005E0AE621A5C6C CRC64;
Query Match 10.0%; Score 71; DB 1; Length 192;
Best Local Similarity 29.5%; Pred. No. 15;
Matches 28; Conservative 9; Mismatches 44; Indels 14; Gaps 4;
OY 22 FDMREALLRVKSSERLALMGCMGHRVLTGTSASAIATVTPKASMLKPPRPOS 81
DB 112 FDCFSAIRKPSLGHIVSPRC-EYQAGHNKVGSLYLALALTTPK---KIKPLPSV 166
OY 82 TKSPELRELSKIREMKNKTISQESARVNHRLPEGH 116
DB 167 KLTEOR-----WNPKQTKGHRGHTM-NGH 192

RESULT 27
HIT_PIG
ID HIT_PIG STANDARD; PRT; 211 AA.
AC P06348;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Histone H1t.
GN H1FT.
OS Euk scrofa (Pig).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=85054795; PubMed=6389534;
RA Cole K.D., York R.G., Kistler W.S.;
RT "The amino acid sequence of boar H1t, a testis-specific H1 histone
variant.";
RL J. Biol. Chem. 259:13695-13702(1984).
CC -!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
CC NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- DEVELOPMENTAL STAGE: THIS HISTONE IS A TESTIS-SPECIFIC H1 VARIANT
CC THAT APPEARS DURING MEIOSIS IN SPERMATOGENESIS.
CC -!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
DR PIR; A02581; HSPG1T.
DR HSP; P08287; 1GHC.
DR InterPro; IPR005818; Histone_H1/H5.
DR InterPro; IPR005819; Histone_H5.
DR Pfam; PF00538; linker_Histone; 1.
DR PRINTS; PR00624; HISTONEH5.
DR SMART; SM00526; H15; 1.
KW Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
KW Acetylation; Spermatogenesis; Testis.
FT MOD_RES 1 ACETYLATION.
FT DOMAIN 39 112 GLOBULAR.
SQ SEQUENCE 211 AA; 22059 MW; EACA47C51A8F5364 CRC64;
Query Match 10.0%; Score 71; DB 1; Length 211;
Best Local Similarity 21.3%; Pred. No. 17;
Matches 27; Conservative 29; Mismatches 49; Indels 22; Gaps 5;
QY 8 TNFAENPTGTFDVMREALLRV-----KSSERLAMLRLACMGHRVL---PGTGAS 59
DB 48 TEALVSQERAGMSLAALKALAAAGYDVKNNGRIKL--GLKSLVGKILVQTRGTGAS 105
QY 60 A---IAATVTPKGSMKLPKPPRPOST-----KSPLELSELRKIRENMKNTISQESAR 107
DB 106 GSFKLKSKAAPEPRKGVKPKAAAKTKKLVLSDSKSPKSAKANKRAKRSRTTAAQKAAR 165
QY 108 VNHRLPE 114
DB 166 SGRKTKE 172
RESULT 28
HSF7_ARATH
ID_HSF7_ARATH STANDARD; PRT; 377 AA.
AC Q9TCD3; Q9SCW3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Heat shock factor protein 7 (HSF 7) (Heat shock transcription factor
7) (HSF 7).
GN HSF7 OR AT4G11660 OR TSC23.90.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RC MEDLINE=20083488; PubMed=10617198;
RA Mayer K.P.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA Pohl T., Dueterhoeft A., Stiekema W., Entian K.-D., Terry N.,
RA Harris B., Ansoerge W., Brandt P., Grivell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermayer B., Maché R., Mueller M.,
RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzneger T., Bothe G., Rampsperger U., Hilbert H., Braun M.,
RA Holzner E., Brandt A., Peters S., van Staveren M., Dirks W.,
RA Moolijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA Bernheiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIay K., Mayes R.,
RA Pettett A., Raandream M.A., Lyne M., Benes V., Rechmann S.,
RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan M., Maarsee A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA Neumann S., Argirou A., Vitale D., Liguori R., Piravandi E.,
RA Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA Chedor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacón D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Sakhon M., Murray J., Sheet P., Schutz K., Huang E., Spiegel L.,
RA Stonking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Grana S., Shouly N., Hasegawa A., Hameed A., Lodi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
thaliana.";
RL Nature 402:769-777(1999).
RN [2]
RP SEQUENCE OF 50-377 FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Green siliques;
RA Schoeffl F., Praendl R.;
RT "De-repression of heat shock protein synthesis in transgenic plants.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DNA-BINDING PROTEIN THAT SPECIFICALLY BINDS HEAT SHOCK
CC PROMOTER ELEMENTS (HSE) AND ACTIVATES TRANSCRIPTION (BY
CC SIMILARITY).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- PTM: EXHIBITS TEMPERATURE-DEPENDENT PHOSPHORYLATION
CC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE HSF FAMILY.
CC -----
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CC -----
CC EMBL; AL049500; CAB39937.1; -.

DR EMBL; AL161532; CAB78209.1; --
DR EMBL; AJ251868; CAB63803.1; --
DR PIR; T04213; T04213.
DR HSSP; P22813; 1HKT.
DR InterPro; IPR000232; HSF_DNA_bind.
DR InterPro; IPR002341; HSF_ETS.
DR Pfam; PF00447; HSF_DNA_bind; 1.
DR PRINTS; PR00056; HSFDOMAIN.
DR ProDom; PD001788; HSF_DNA_bind; 1.
DR SMART; SM00415; HSF; 1.
DR PROSITE; PS00434; HSF_DOMAIN; 1.
KW Transcription regulation; Nuclear protein; DNA-binding; Activator;
Phosphorylation; Heat shock; Multigene family.
FT DNA_BIND 57 151 BY SIMILARITY.
FT DOMAIN 14 21 POLY-GLY.
FT DOMAIN 32 50 POLY-GLY.
FT DOMAIN 155 171 POLY-ALA.
FT DOMAIN 202 207 POLY-ALA.
FT CONFLICT 50 50 G -> R (IN REF. 2).
FT SEQUENCE 377 AA; 39705 MW; FDI5ES95B7FC584 CRC64;

Query Match 10.0%; Score 71; DB 1; Length 377;
Best Local Similarity 28.4%; Pred. No. 34;
Matches 27; Conservative 14; Mismatches 24; Indels 30; Gaps 5;

QY 54 PGTGASAIATVTPKGASMKLPPRQSTKSPFLRLSKIRENMNTISQESARVN--- 109
Db 201 PAAAAAAGGV--GGSLQ-----RTTCTTAPLVEENRERLKNRLEKMTLKGILY 254
QY 110 -----HRLPEGHP--LLEKRAE 124
Db 255 ANIYTLMAVTFQEQDCALHPGKPLDLLPERQE 289

RESULT 29
APGM_PYRAB STANDARD; PRT; 410 AA.
ID APGM_PYRAB
AC Q9V2N6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (aPGAM).
GN APGM OR PYRAB00490 OR PAR2318.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GS5 / Orsay;
RX PubMed=12622808;
RA Cohen G.N., Barbe V., Flament D., Galperin M., Heilig R., Lecompte O.,
RA Poch O., Prieur D., Querellou J., Ripp R., Thierry J.-C.,
RA Van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
RT "An integrated analysis of the genome of the hyperthermophilic
archaeon Pyrococcus abyssi.";
RL Mol. Microbiol. 47:1495-1512(2003).
CC -!- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate (By similarity).
CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
CC -!- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY. A-PGAM SUBFAMILY.
CC
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CC
DR EMBL; AJ248283; CAB48972.1; --

DR PIR; E75190; E75190.
DR HAMAP; MF_01402; --; 1.
DR InterPro; IPR004456; BcpB.
DR InterPro; IPR006124; Metalloenzyme.
DR Pfam; PF01676; Metalloenzyme; 1.
DR ProDom; PD004704; BcpB; 1.
DR TIGRFAMs; TIGR003106; bcpB; 1.
KW Isomerase; Complete proteome.
SQ SEQUENCE 410 AA; 45201 MW; 91C8A89637608826 CRC64;

Query Match 10.0%; Score 71; DB 1; Length 410;
Best Local Similarity 22.7%; Pred. No. 37;
Matches 29; Conservative 21; Mismatches 52; Indels 26; Gaps 4;

QY 13 ENRFTFGTDFDVMREALL-----RVKSSRLMLRAL-----AGMCGHRVLP 54
Db 91 EDDLAFRVNFATLKGIVVDRAGRISTEAHELAKEIQEVDVGVDFIFKATGCHRAVL 150
QY 55 GTGASAIATVTPKGASMKLPPRQSTKSPFLRLSKIRENMNTISQESARVNHRLPE 114
Db 151 VLKGMADGYRVGNDPDHVGKPKPHKFSWEDEE-----SKKVAE-----ILEEFVKKAEVLE 202
QY 115 GHPLLEKR 122
Db 203 RHPINEKR 210

RESULT 30
APGM_PYRFU STANDARD; PRT; 411 AA.
ID APGM_PYRFU
AC P58814;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase
DE (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (aPGAM).
GN APGM OR PF1959.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP CHARACTERIZATION.
RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
RX MEDLINE=22071963; PubMed=12076795;
RA van der Oost J., Huynen M.A., Verhees C.H.;
RT "Molecular characterization of phosphoglycerate mutase in archaea.";
RL FEMS Microbiol. Lett. 212:111-120(2002).
CC -!- FUNCTION: Catalyzes the interconversion of 2-phosphoglycerate and
CC 3-phosphoglycerate.
CC -!- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = 3-phospho-D-glycerate.
CC -!- COFACTOR: Magnesium (Probable).
CC -!- ENZYME REGULATION: Inhibited to approximately 20% by EDTA.
CC -!- SUBUNIT: Homotetramer (Probable).
CC -!- MISCELLANEOUS: Optimal pH is 8.0.
CC -!- SIMILARITY: BELONGS TO THE BPG-INDEPENDENT PHOSPHOGLYCERATE MUTASE
CC FAMILY. A-PGAM SUBFAMILY.
CC
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CC
DR EMBL; AE010289; AAL82083.1; --

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DR HAMAP; MF_01402; -; 1.
DR InterPro; IPR004456; BcbP.
DR InterPro; IPR006124; Metalloenzyme.
DR Pfam; PF01676; Metalloenzyme; 1.
DR ProDom; PD004704; BcbP; 1.
DR TIGRFAMs; TIGR00306; bcbP; 1.
KW Isomerase; Magnesium; Complete proteome.
SQ SEQUENCE 411 AA; 45314 MW; 870587E630C2B104 CRC64;

Query Match 10.0%; Score 71; Length 411;
Best Local Similarity 26.2%; Pred. No. 37;
Matches 28; Conservative 14; Mismatches 39; Indels 26; Gaps 5;

QY 31 RVKSERLAMLRL-----AGMCHR---VLPGTGASAIATVTPKGSMKLK 75
D 116 RSTEEAHELAKAQNVDIIFGATGHRVILVKGNAEGYKGVNDPHEAG---K 172
QY 76 PPRFQSTKSPELRELSKIREMNKTIQSARVNHRLPEGHPLLEKR 122
D 173 FPHFTWED----EASKVAE----ILEEFVKAHEVLDRHPINEXR 211

RESULT 31
RNE_ECOLI
ID -RNE_ECOLI STANDARD; PRT; 1061 AA.
AC P21513; P77591;
DT 01-MAY-1991 (Rel. 18; Created)
DT 15-JUL-1998 (Rel. 35; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Ribonuclease E (EC 3.1.4.-) (RNase E).
GN RNE OR AMS OR HMP1 OR E1084.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97061202; PubMed=8905232;
RA Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
RA Sanpei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [3]
RP SEQUENCE OF 1-1025 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=93078265; PubMed=1447789;
RA Casaregola S., Jacq A., Lacud D., McGurk G., Margaron S.,
RA Tempete M., Norris V., Holland I.B.;
RT "Cloning and analysis of the entire Escherichia coli ams gene. ams is
RT identical to hmp1 and encodes a 114 kDa protein that migrates as a
RT 180 kDa protein.";
RL J. Mol. Biol. 228:30-40(1992).
RN [4]
RP SEQUENCE OF 1-844 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=91131576; PubMed=1704367;
RA Claverie-Martin F., Diaz-Torres M., Yancey S.D., Kushner S.R.;
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RT "Analysis of the altered mRNA stability (ams) gene from Escherichia
RT coli. Nucleotide sequence, transcriptional analysis, and homology of
RT its product to MRP3, a mitochondrial ribosomal protein from
RT Neurospora crassa.";
RL J. Biol. Chem. 266:2843-2851(1991).
RN [5]
RP PARTIAL SEQUENCE FROM N.A., AND SEQUENCE OF 1-27.
RC STRAIN=K12;
RX MEDLINE=91187608; PubMed=2011493;
RA Chauhan A.K., Miczak A., Taraseviciene L., Apirion D.;
RT "Sequencing and expression of the rne gene of Escherichia coli.";
RL Nucleic Acids Res. 19:125-129(1991).
RN [6]
RP SEQUENCE OF 844-1061 FROM N.A., AND CHARACTERIZATION.
RC STRAIN=K12;
RX MEDLINE=94022304; PubMed=8415644;
RA Cormack R.S., Genereux J.L., Mackie G.A.;
RT "RNase E activity is conferred by a single polypeptide:
RT overexpression, purification, and properties of the ams/rne/hmp1 gene
RT product.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:9006-9010(1993).
RN [7]
RP CHARACTERIZATION.
RX Walsh A.P., Tock M.R., Mallen M.H., Kabardin V.R., Gabain Av A.,
RA McDowall K.J.;
RT "Cleavage of poly(A) tails on the 3'-end of RNA by ribonuclease E of
RT Escherichia coli.";
RL Nucleic Acids Res. 29:1864-1871(2001).
CC -1- FUNCTION: MATURES 5S RNA FROM ITS PRECURSORS FROM ALL THE RNA
CC GENES. IT ALSO CLEAVES RNA I, A MOLECULE THAT CONTROLS THE
CC REPLICATION OF COLE1 PLASMID DNA. IT IS THE MAJOR ENDOBIONUCLEASE
CC PARTICIPATING IN MRNA TURNOVER IN E.COLI. IT INITIATES THE DECAY
CC OF RNAs BY CUTTING THEM INTERNALLY NEAR THEIR 5'-END. IT IS ABLE
CC TO REMOVE POLY(A) TAILS BY AN ENDOUCLEOLYTIC PROCESS.
CC -1- SUBUNIT: ORGANIZED INTO A STRUCTURE (PROCESOME OR RNA
CC DEGRADOSOME) CONTAINING A NUMBER OF RNA-PROCESSING ENZYMES.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE RNE FAMILY.
CC -1- SIMILARITY: Contains 1 SI motif domain.
CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 1003
CC ONWARD AND IS SHORTER (1025 AA) DUE TO A FRAMESHIFT.
CC -1- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN IN THE C-TERMINUS
CC AND IS SHORTER (815 AA) DUE TO A FRAMESHIFT.
CC -1- CAUTION: REF.5 SEQUENCE WAS ALSO INCORRECT IN MANY POSITIONS DUE
CC TO FRAMESHIFTS.
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CC -----
DR EMBL; A5000209; AAC74168.1; -
DR EMBL; D90744; BAA35893.1; -
DR EMBL; X67470; CAA47818.1; ALT_FRAME.
DR EMBL; M62747; AAA23443.1; ALT_FRAME.
DR EMBL; X54309; AAA38206.1; ALT_FRAME.
DR EMBL; L23942; AAA03347.1; -
DR PIR; A64852; S27311.
DR EcoGene; EGI0859; rne.
DR InterPro; IPR004659; RNaseEG.
DR InterPro; IPR003029; S1.
DR Pfam; PF00575; S1; 1.
DR SMART; SM00316; S1; 1.
DR TIGRFAMs; TIGR00757; RNaseEG; 1.
DR PROSITE; PS50126; S1; 1.
KW Hydrolase; Nuclease; Endonuclease; RNA-binding; Complete proteome.
FT DOMAIN 39 119 SI MOTIF.
FT STRAIN=K12;
FT MEDLINE=91131576; PubMed=1704367;
FT Claverie-Martin F., Diaz-Torres M., Yancey S.D., Kushner S.R.;
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FT CONFLICT 564 564 A -> R (IN REF. 3).
FT CONFLICT 784 784 N -> K (IN REF. 3).
FT CONFLICT 838 838 A -> R (IN REF. 4).
FT CONFLICT 905 905 P -> R (IN REF. 3).
FT CONFLICT 1048 1048 H -> R (IN REF. 6).
SQ SEQUENCE 1061 AA; 118182 MW; B911877DF03E79A8 CRC64;

Query Match 10.0%; Score 71; DB 1; Length 1061;
Best Local Similarity 21.7%; Pred.No. 1.2e+02;
Matches 25; Conservative 44; Indels 24; Gaps 13;

QY 9 NFVAENRPTGETFDVNRREALRVKSSERLAMLRLALMGCMGHRVLPGTGASAIATAATPTPK 68
Db 81 NYSAGHRPNKIKDLVREGQEVQIDKEE-----GNKGAALTTFISLA 123
QY 69 GASKMLKPPRPQSTKSPELRSKRLKREMKNTISQESARYNHRLPFGHPLEKKA 123
Db 124 GSYLVLP-----NPRAGIGSRREGDRTTELKE-ALASLELPFGNGLIVRTA 171

RESULT 32
PTNE_MOUSE
ID PTNE_MOUSE STANDARD; PRT; 1189 AA.
AC O62130;
DC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
DE Protein-tyrosine phosphatase PTP36).
DE PTPN14.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=CB-17-SCID; TISSUE=Thymus;
RP MEDLINE=94354845; PubMed=8074693;
RA Sawada M., Ogata M., Fujino Y., Hamaoka T.;
RT "CDNA cloning of a novel protein tyrosine phosphatase with homology
RT to cytoskeletal protein 4.1 and its expression in T-lineage cells.";
RL Biochem Biophys Res Commun. 203:479-484(1994).
CC 1- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF T CELL DEVELOPMENT.
CC 1- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC 1- TISSUE SPECIFICITY: THYMUS; IN CELLS OF BOTH HEMATOPOIETIC AND
CC NON-HEMATOPOIETIC ORIGINS.
CC 1- SIMILARITY: Contains 1 FERM domain.
CC 1- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D31842; BAA06628.1; ..
CC PIR; JC2366; JC2386.
CC HSSP; Q06124; 2SHP.
CC
CC MGD; MGI:102467; Ptpn14.
CC InterPro; IPR000299; Band 4.1.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00373; Band 41; 1.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PRO0935; BAND41.
CC PRINTS; PRO0700; PRTYPHPHTASE.
CC SMART; SM00295; B41; 1.
CC SMART; SM00194; PTPC; 1.
CC PROSITE; PS00660; FERM 1; 1.

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DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS0057; FERM_3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
DR PROSITE; PS00506; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00506; TYR_PHOSPHATASE_2; 1.
KW Structural protein; Cytoskeleton; Hydrolase.
FT DOMAIN 21 306 FERM.
FT DOMAIN 935 1189 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 1123 1123 BY SIMILARITY.
FT DOMAIN 566 573 POLY-PRO.
FT DOMAIN 635 639 POLY-GLY.
FT DOMAIN 712 718 POLY-GLU.
SQ SEQUENCE 1189 AA; 135030 MW; 2B85BE5F9C723303 CRC64;

Query Match 10.0%; Score 71; DB 1; Length 1189;
Best Local Similarity 26.0%; Pred.No.1.3e+02;
Matches 26; Conservative 19; Mismatches 17; Indels 38; Gaps 5;

QY 48 CQHRLVPGTGASAIATV-TPKGASKLK-----PPRPQ---STKS 84
Db 522 CAMPIKP-GASSISHTVSTPELANNQLQAQHYSTAHMLKNVLFRRPPPPYRPRPAIST 579
QY 85 PEURE-----LSRKIRENMKNTISQBSARVNH 111
Db 580 PDLASHRHKKVYSGSPDLVTRKRVQLSVKTFQEDSPVAVHQ 619

RESULT 33
ZDS_MAIZE
ID ZDS_MAIZE STANDARD; PRT; 570 AA.
AC Q92TP4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Zeta-carotene desaturase, chloroplast precursor (EC 1.14.99.30)
DE (Carotene 7,8-desaturase).
GN ZDS1 OR ZDS.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID:4577;
RN [1]
SEQUENCE FROM N.A.
RA Luo R., Wurtzel E.T.;
RT "A maize cDNA encoding zeta carotene desaturase.";
RL (In) Plant Gene Register PGR99-118.
CC -!- FUNCTION: Catalyzes the conversion of zeta-carotene to lycopene
CC via the intermediary of neurosporene. It carries out two
CC consecutive desaturations (introduction of double bonds) at
CC positions C-7 and C-7'.
CC -!- CATALYTIC ACTIVITY: Zeta-carotene + AH(2) + O(2) = neurosporene +
CC A + 2 H(2)O.
CC -!- CATALYTIC ACTIVITY: Neurosporene + AH(2) + O(2) = lycopene + A + 2
CC H(2)O.
CC -!- COFACTOR: NAD, NADP, OR FAD (PROBABLE).
CC -!- PATHWAY: Carotenoid biosynthesis.
CC -!- SUBCELLULAR LOCATION: Chloroplast; chromoplast.
CC -!- SIMILARITY: BELONGS TO THE ZETA CAROTENE DESATURASE FAMILY.
CC
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CC
CC EMBL; AF047490; RAD02462.1;
DR InterPro; IPR000759; Adnrdx_reductase.
DR InterPro; IPR002937; Amino_Oxidase.
DR Pfam; PF01593; Amino_oxidase; 1.
DR PRINTS; PR00419; ADXEDTASE.

```

KW Carotenoid biosynthesis; Oxidoreductase; NAD; Flavoprotein; FAD;
KW Chloroplast; Transit peptide.
FT TRANSIT 1 CHLOROPLAST (POTENTIAL).
FT CHAIN ? 570 ZETA-CAROTENE DESATURASE.
SQ SEQUENCE 570 AA; 63127 MW; C7AD8F2FD6253128 CRC64;

Query Match 10.0%; Score 70.5; DB 1; Length 570;
Best Local Similarity 34.1%; Pred. No. 61;
Matches 29; Conservative 11; Mismatches 26; Indels 19; Gaps 6;

QY 51 RVLPTGTG-----ASAIAA--TVTP---KGASMKLKPPOSTKSPELRELSRKIREMNK 99
Db 18 RARFCTGLVPPRRASAVARSTVSPWRQSRQLFPPEPHYRGPKL-----KVAIGA 72

QY 100 TISOESARVNHRLPEGH--PILKPR 122
Db 73 GLAGMSTAV-ELLDOGHVEVDLYSR 96

RESULT 34
TCOF_HUMAN
ID TCOF_HUMAN STANDARD; PRT; 1411 AA.
AC Q13428; Q99408; Q99860;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Treacle protein (Treacher Collins syndrome protein).
GN TCOF1
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96154183; PubMed=8563749;
RA Dixon J., Edwards S.J., Gladwin A.J., Dixon M.J., Loftus S.K.,
RA Bomer C.A., Koprivnikar K., Wasmuth J.J.;
RT "Positional cloning of a gene involved in the pathogenesis of
Treacher Collins syndrome."
RL Nat. Genet. 12:130-136(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97228900; PubMed=9074926;
RA Dixon J., Edwards S.J., Anderson I., Brass A., Scambler P.J.,
RA Dixon M.J.;
RT "Identification of the complete coding sequence and genomic
organization of the Treacher Collins syndrome gene."
RL Genome Res. 7:223-234(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=97250498; PubMed=90963354;
RA Wise C.A., Chiang L.C., Paznekas W.A., Sharma M., Musy M.M.,
RA Ashley J.A., Lovett M., Jabs E.W.;
RT "TCOF1 gene encodes a putative nucleolar phosphoprotein that exhibits
mutations in Treacher Collins syndrome throughout its coding
region."
RL Proc. Natl. Acad. Sci. U.S.A. 94:3110-3115(1997).
RN [4]
RP VARIANTS LEU-439; VAL-810; VAL-1313 AND GLY-1355, AND VARIANT TCS
ARG-53.
RX MEDLINE=97195537; PubMed=9042910;
RA Edwards S.J., Gladwin A.J., Dixon M.J.;
RT "The mutational spectrum in Treacher Collins syndrome reveals a
predominance of mutations that create a premature-termination
codon."
RL Am. J. Hum. Genet. 60:515-524(1997).
CC -1- DISEASE: Defects in TCOF1 are the cause of Treacher Collins
syndrome (TCS) [MIM:154500]. TCS is an autosomal dominant disorder
of craniofacial development that occurs with an incidence of
1/50,000 live births. The clinical features of TCS are bilaterally
symmetrical and include: (1) abnormalities of the external ears
atresia of the external ear canals, and malformation of the middle
ear ossicles, which may result in conductive hearing loss; (2)

CC lateral downward sloping of palpebral fissures, frequently with
CC colobomas of the lower eyelids; (3) hypoplasia of the mandible and
CC zygomatic complex; (4) cleft palate.
CC -1- SIMILARITY: Contains 1 Lish domain.
CC -----
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CC -----
CC EMBL; U40847; AAC50903.1; -
CC EMBL; U76366; AAC51181.1; -
CC EMBL; U84664; AAC51185.1; -
CC EMBL; U84640; AAC51185.1; JOINED.
CC EMBL; U84641; AAC51185.1; JOINED.
CC EMBL; U84642; AAC51185.1; JOINED.
CC EMBL; U84643; AAC51185.1; JOINED.
CC EMBL; U84644; AAC51185.1; JOINED.
CC EMBL; U84645; AAC51185.1; JOINED.
CC EMBL; U84646; AAC51185.1; JOINED.
CC EMBL; U84647; AAC51185.1; JOINED.
CC EMBL; U84648; AAC51185.1; JOINED.
CC EMBL; U84649; AAC51185.1; JOINED.
CC EMBL; U84650; AAC51185.1; JOINED.
CC EMBL; U84651; AAC51185.1; JOINED.
CC EMBL; U84652; AAC51185.1; JOINED.
CC EMBL; U84653; AAC51185.1; JOINED.
CC EMBL; U84654; AAC51185.1; JOINED.
CC EMBL; U84655; AAC51185.1; JOINED.
CC EMBL; U84656; AAC51185.1; JOINED.
CC EMBL; U84657; AAC51185.1; JOINED.
CC EMBL; U84658; AAC51185.1; JOINED.
CC EMBL; U84659; AAC51185.1; JOINED.
CC EMBL; U84660; AAC51185.1; JOINED.
CC EMBL; U84661; AAC51185.1; JOINED.
CC EMBL; U84662; AAC51185.1; JOINED.
CC EMBL; U84663; AAC51185.1; JOINED.
CC EMBL; U79659; AAB40722.1; -
CC EMBL; U79645; AAB40722.1; JOINED.
CC EMBL; U79646; AAB40722.1; JOINED.
CC EMBL; U79647; AAB40722.1; JOINED.
CC EMBL; U79648; AAB40722.1; JOINED.
CC EMBL; U79649; AAB40722.1; JOINED.
CC EMBL; U79650; AAB40722.1; JOINED.
CC EMBL; U79651; AAB40722.1; JOINED.
CC EMBL; U79652; AAB40722.1; JOINED.
CC EMBL; U79653; AAB40722.1; JOINED.
CC EMBL; U79654; AAB40722.1; JOINED.
CC EMBL; U79655; AAB40722.1; JOINED.
CC EMBL; U79656; AAB40722.1; JOINED.
CC EMBL; U79657; AAB40722.1; JOINED.
CC EMBL; U79658; AAB40722.1; JOINED.
CC Genew; HGNC:11654; TCOF1.
CC MIM; 606847; -
CC MIM; 154500; -
CC GO; GO:0005730; C:nucleolus; TAS.
CC GO; GO:0005215; P:transporter activity; TAS.
CC GO; GO:0001501; P:skeletal development; TAS.
CC InterPro; IPR006594; Lish.
CC InterPro; IPR003993; treacle.
CC Pfam; PF03546; treacle; 3.
CC PRINTS; PRO1503; TREACLE.
CC SMART; SM00667; Lish; 1.
CC PROSITE; PS00896; Lish; 1.
CC Disease mutation; Polymorphism.
CC FT DOMAIN 6 38 LISH.
CC FT DOMAIN 89 97 POLY-GLU.
CC FT DOMAIN 204 207 POLY-SER.
CC FT DOMAIN 616 619 POLY-SER.
CC FT DOMAIN 919 924 POLY-SER.

FT DOMAIN 1285 1289 POLY-LYS.
FT DOMAIN 1375 1386 POLY-LYS.
FT DOMAIN 1398 1405 POLY-LYS.
FT VARIANT 53 53 W -> R (in TCS).
FT VARIANT 439 439 /FTId=VAR_005630.
FT VARIANT 810 810 P -> L.
FT VARIANT 1313 1313 /FTId=VAR_005631.
FT VARIANT 1355 1355 A -> V.
FT VARIANT 1313 1313 /FTId=VAR_005632.
FT VARIANT 1355 1355 A -> V (in dbSNP:15251).
FT VARIANT 1313 1313 /FTId=VAR_005633.
FT VARIANT 1355 1355 D -> G.
FT VARIANT 1312 1312 /FTId=VAR_005634.
FT VARIANT 1411 1411 K -> Q (IN REF. 2).
FT CONFLICT 1411 1411 MW; 38802030985C2699 CRC64;
SQ SEQUENCE 1411 AA; 144312 MW; 38802030985C2699 CRC64;

Query Match 10.0%; Score 70.5; DB 1; Length 1411;
Best Local Similarity 21.2%; Pred. No. 1.8e+02;
Matches 31; Conservative 19; Mismatches 47; Indels 49; Gaps 5;

QY 5 STTTNVAENR-----PTG-----ETFDVMEALLRVKSSERLAML 41
DB 164 SANTTLVSETEEGSVPAFGAAAKPMWAGADSSSDTSSSDTDEVEKASEKILQV 223
QY 42 RALAGMCHRVLPFGTGASAIATVTPKG---ASMKLKPPRFQSTKSPPELRELSRKIREM 97
DB 224 RAASA-----PAKGTGPGKATPAPPKAGAVASQTKAGKE-----ED 261
QY 98 NKTISQESARVNHRLPEGHFILLEKRA 123
DB 262 SSSSESSSEETPAAKLIQAKA 287

RESULT 35
PNHJ_ECOLI
ID_PNHJ_ECOLI STANDARD; PRT; 281 AA.
AC P16688;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE PNHJ protein.
GN PNHJ OR B4098.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=91193228; PubMed=1840580;
RA Makino K., Kim S.K., Shinagawa H., Amemura M., Nakata A.;
RT "Molecular analysis of the cryptic and functional phn operons for
phosphonate use in Escherichia coli K-12.";
RL J. Bacteriol. 173:2665-2672(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=95334362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
region from 92.8 through 100 minutes.";
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=B.
RX MEDLINE=90170953; PubMed=2155230;
RA Chen C.-M., Ye Q.-Z., Zhu Z., Wanner B.L., Walsh C.T.;
RT "Molecular biology of carbon-phosphorus bond cleavage. Cloning and
sequencing of the phn (psid) genes involved in alkylphosphonate
uptake and C-P lyase activity in Escherichia coli B.";
RL J. Biol. Chem. 265:4461-4471(1990).
CC -!- FUNCTION: BELONGS TO AN OPERON INVOLVED IN ALKYLPHOSPHONATE

CC UPTAKE AND C-P LYASE. EXACT FUNCTION NOT KNOWN.
CC -!- MISCELLANEOUS: THE SEQUENCE SHOWN IS THAT OF STRAIN K12.
CC -!- SIMILARITY: BELONGS TO THE PNHJ FAMILY.
CC -----
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CC -----
DR EMBL; D90227; BAA14270.1; -;
DR EMBL; U14003; AAN96997.1; -;
DR EMBL; AE000482; AAC77059.1; -;
DR EMBL; J05260; AAA24348.1; -;
DR PIR; A65219; A65219.
DR EcoGene; EG10719; phnJ.
KW Alkylphosphonate uptake; Complete proteome.
FT VARIANT 103 103 V -> L (IN STRAIN B)
SQ SEQUENCE 281 AA; 31845 MW; 241F6AF140995468 CRC64;

Query Match 9.9%; Score 70; DB 1; Length 281;
Best Local Similarity 23.8%; Pred. No. 29;
Matches 36; Conservative 27; Mismatches 52; Indels 36; Gaps 8;

QY 19 GETFDVMEALLRVKSSERLAMLALAGMCHRV-----LP---GTGASAIATVTP 67
DB 6 GYNFAYLDE---QTKMIRRAILKAVA-IPGYQVFGREMPYMGWGTGIGLTASVIG 61
QY 68 KGASMK-LKPPRQSTKSPPELRELSRKIRENMKNTISQESARV---NHLRPE----- 114
DB 62 ESDVLKVIDQADDTTNAVSIKFNFFKVTGVTGTTERTDDATVQTRHRIPTLPTEDQII 121
QY 115 -----GHPL--LEKRAEYFHLRLSLKASQGV 137
DB 122 IFQVPIPEPLRFIPRETETRTMHALEEYGV 152

RESULT 36
CREM_CANFA
ID_CREM_CANFA STANDARD; PRT; 344 AA.
AC P79145;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE CAMP responsive element modulator.
GN CREM.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RX MEDLINE=97410117; PubMed=9266932;
RA Uyttersprot N., Miot F.;
RT "Dog CREM transcription factors: cloning, tissue distribution, and
RT identification of new isoforms.";
RL Biochem. Biophys. Res. Commun. 237:74-78(1997).
CC -!- FUNCTION: THIS PROTEIN BINDS THE CAMP RESPONSE ELEMENT (CRE), A
CC SEQUENCE PRESENT IN MANY VIRAL AND CELLULAR PROMOTERS. CREM ALPHA,
CC BETA, AND GAMMA ISOFORMS ARE ANTAGONISTS OF THE CAMP
CC TRANSCRIPTIONAL RESPONSE, WHILE THE DELTA ISOFORM IS AN ACTIVATOR.
CC -!- SUBUNIT: Birds DNA as a dimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Belta;
CC IsoId=P79145-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=P79145-2; Sequence=Not described;
CC Name=Beta;

```

CC AND GAMMA.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the cation transport ATPases family (P-type
CC ATPases). Subfamily IIC.
CC -----
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CC -----
CC EMBL; M59959; AAA48981.1; --
CC PIR; I50394; A37227.
CC HSP; P04191; LEUL.
CC -----
CC InterPro; IPR001757; ATPase_E1-E2.
CC InterPro; IPR006069; Cation_ATPase.
CC InterPro; IPR006068; Cation_ATPase_C.
CC InterPro; IPR004014; Cation_ATPase_N.
CC InterPro; IPR005834; Hydrolase.
CC InterPro; IPR005775; Na/K_ATPase_alph.
CC Pfam; PF00689; Cation_ATPase_C; 1.
CC Pfam; PF00690; Cation_ATPase_N; 1.
CC Pfam; PF00122; E1-E2_ATPase_1.
CC Pfam; PF00702; Hydrolase; 1.
CC PRINTS; PRO0119; CATATPASE.
CC PRINTS; PRO0121; NAKATPASE.
CC TIGRFAMs; TIGR01106; ATPase-IIC X-K; 1.
CC TIGRFAMs; TIGR01494; ATPase P-type; 5.
CC PROSITE; PS00154; ATPase_E1-E2; 1.
CC Hydrolase; Sodium/potassium transport; Transmembrane; Phosphorylation;
CC Magnesium; Metal-binding; ATP-binding; Multigene family.
CC DOMAIN 1 82 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 83 103 POTENTIAL.
CC DOMAIN 104 126 LUMENAL (POTENTIAL).
CC TRANSMEM 127 147 POTENTIAL.
CC DOMAIN 148 283 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 284 303 POTENTIAL.
CC DOMAIN 304 315 LUMENAL (POTENTIAL).
CC TRANSMEM 316 333 POTENTIAL.
CC DOMAIN 334 766 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 767 786 POTENTIAL.
CC DOMAIN 787 796 LUMENAL (POTENTIAL).
CC TRANSMEM 797 817 POTENTIAL.
CC DOMAIN 818 837 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 838 860 POTENTIAL.
CC DOMAIN 861 912 LUMENAL (POTENTIAL).
CC TRANSMEM 913 932 POTENTIAL.
CC DOMAIN 933 945 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 946 964 POTENTIAL.
CC DOMAIN 965 979 LUMENAL (POTENTIAL).
CC TRANSMEM 980 1000 POTENTIAL.
CC DOMAIN 1001 1017 CYTOPLASMIC (POTENTIAL).
CC MOD_RES 371 371 PHOSPHORYLATION (BY SIMILARITY).
CC MOD_RES 937 937 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
CC BINDING 77 79 BINDING OF PHOSPHOINOSITIDE-3 KINASE (BY
CC METAL 711 711 SIMILARITY).
CC METAL 715 715 MAGNESIUM (BY SIMILARITY).
CC BINDING 502 502 MAGNESIUM (BY SIMILARITY).
CC SEQUENCE 1017 AA; 112050 MW; 38E87C1BDE93B8C5 CRC64;
CC -----
CC Query Match 9.9%; Score 70; DB 1; Length 1017;
CC Best Local Similarity 25.0%; Pred No. 14e-02;
CC Matches 40; Conservative 12; Mismatches 50; Indels 58; Gaps 7;
CC -----
CC 3 STST-----TTTFVAENRPTF-----
CC 364 STSTICSDKTCGTLTQNRMTVAHMFNQHIEADTTDOSGATFD-----
CC 40 MLRALAGMCHRVL-PGTGASAIATVTPKGA-----MKLKKPPQSTK 83
CC -----
CC QY
CC DB
CC QY

```

Db 415 ALSRIAGCNRAVFKPGGENTISIKRDTAGDASESALKLCIQLSCGVSXKVKRDKNPKVTE 474

Qy 84 SPELRLSRKIRENMKTTISQESARVNHRLPECHPLLEKRA 123

Db 475 IP-----FNSTYK--YQLSIHEREDPQGHILVMKGA 504

RESULT 38

SMC3 YEAST

ID SMC3 YEAST STANDARD; PRT: 1230 AA.

AC P47037;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Structural maintenance of chromosome 3 (DA-Box protein SMC3).

GN SMC3 OR YJL074C OR J1049.

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.

OX NCBI_TaxID:4932;

RN SEQUENCE FROM N.A.

RP STRAIN=W303;

RC MEDLINE=97474309; PubMed=9335333;

RX Michaelis C., Ciosk R., Nasmyth K.;

RA "Cohesins: chromosomal proteins that prevent premature separation of

RT sister chromatids";

RL Cell 91:35-45(1997).

RN SEQUENCE FROM N.A.

RP Rose M., Koetter P., Enrian K.D.;

RA Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.

RL [3]

RP SEQUENCE FROM N.A.

RC STRAIN=S288c / FY1678;

RA Sor F.J.;

RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.

RN [4]

RP IDENTIFICATION IN A COHESIN COMPLEX WITH SMC1; IRR1 AND MCD1, AND

RP INTERACTION OF THE COHESIN COMPLEX WITH SCC2.

RX PubMed=9990856;

RA Toth A., Ciosk R., Uhlmann F., Galova M., Schleiffer A., Nasmyth K.;

RT "yeast Cohesin complex requires a conserved protein, Eco1p(Ctf7), to

RL establish cohesion between sister chromatids during DNA replication.";

RL Genes Dev. 13:320-333(1999).

RN [5]

RP IDENTIFICATION IN A COHESIN COMPLEX WITH SMC3; MCD1 AND IRR1, AND

RP STRUCTURE.

RX PubMed=11983169;

RA Haering C.H., Loewe J., Hochwagen A., Nasmyth K.;

RT "Molecular architecture of SMC proteins and the yeast cohesin

RL complex.";

RL Mol. Cell 9:773-788(2002).

CC -!- FUNCTION: Involved in chromosome cohesion during cell cycle and in

CC DNA repair. Central component of cohesin complex. The cohesin

CC complex is required for the cohesion of sister chromatids after

CC DNA replication. The cohesin complex apparently forms a large

CC proteinaceous ring within which sister chromatids can be trapped.

CC At anaphase, the complex is cleaved and dissociates from

CC chromatin, allowing sister chromatids to segregate.

CC -!- SUBUNIT: Cohesin complexes are composed of the SMC1 and SMC3

CC heterodimer attached via their hinge domain, MCD1/SCC1 which link

CC them, and IRR1/SCC3, which interacts with MCD1. The cohesin

CC complex also interacts with SCC2, which is required for its

CC association with chromosomes.

CC -!- SUBCELLULAR LOCATION: Nuclear protein. Associates with chromatin.

CC Before prophase it is scattered along chromosome arms. At

CC anaphase, the MCD1 subunit of the cohesin complex is cleaved,

CC leading to the dissociation of the complex from chromosomes,

CC allowing chromosome separation.

CC -!- DOMAIN: The flexible hinge domain, which separates the large

CC intramolecular coiled coil regions, allows the heterotypic

CC interaction with the corresponding domain of SMC1, forming a V-

shaped heterodimer. The two heads of the heterodimer are then

connected by different ends of the cleavable MCD1 protein, forming

a ring structure (By similarity).

-!- SIMILARITY: Belongs to the SMC family. SMC3 subfamily.

CC

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CC

EMBL; Y14278; CAA74655.1; -;

DR EMBL; Z49349; CAA89366.1; -;

DR EMBL; X88851; CAA61313.1; -;

DR PIR; S56850; S56850.

DR SGD; S0003610; SMC3.

DR GO; GO:0007151; P:sporulation (sensu Saccharomycetes); IMP.

DR GO; GO:0007130; P:synaptonemal complex formation; IMP.

DR InterPro; IPR003405; SMC_C.

DR InterPro; IPR003395; SMC_N.

DR Pfam; PF02463; SMC_N; 1.

DR Pfam; PF02483; SMC_C; 1.

KW Mitosis; Cell cycle; Chromosome partition; ATP-binding; Coiled coil;

FT NP_BIND 32 39 ATP (POTENTIAL).

FT DOMAIN 172 482 COILED COIL (POTENTIAL).

FT DOMAIN 483 684 FLEXIBLE HINGE.

FT DOMAIN 685 1041 COILED COIL (POTENTIAL).

FT DOMAIN 1126 1161 ALA/ASP-RICH (DA-BOX).

SEQ SEQUENCE 1230 AA; 141336 MW; B152D88F7780341F CRC64;

Query Match 9.9%; Score 70; DB 1; Length 1230;

Best Local Similarity 25.9%; Pred. No. 1.7e+02;

Matches 29; Conservative 21; Mismatches 42; Indels 20; Gaps 4;

Qy 27 EALLRVKSSERL--AMLRALAGMCHRVLPCTGASAIATVTPKGASMKLKPQPTKTS 84

Db 285 EASLKRNATDLQAKLR-----EESISQKLT--NVNKKIDVQQQIESN 327

Qy 85 PELREL-SRKIRENMKTTISQESARVNHRLPECHPLLEKRAEYFRHLASLSKSQ 135

Db 328 BEQRNLSATLKEIKTSIEQRKQKLSKILPRYQELTKEEAMYLQLASLOOK 379

RESULT 39

VSIB TRYBB

ID VSIB TRYBB STANDARD; PRT: 471 AA.

AC P07208;

DT 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Variant surface glycoprotein ILTAT 1.1BC precursor (VSG).

OS Trypanosoma brucei brucei

OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.

OX NCBI_TaxID=5702;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=82245585; PubMed=6927851;

RA Rice-Ficht A.C., Chen K.K., Donelson J.E.;

RT "Point mutations during generation of expression-linked extra copy of

RT trypanosome surface glycoprotein gene.";

RL Nature 298:676-679(1982).

CC -!- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF THE PARASITE. THE

CC TRYPAOSOME EVADES THE IMMUNE RESPONSE OF THE HOST BY EXPRESSING

CC A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM AN ESTIMATED 1000

CC VSG GENES.

CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.

CC A SOLUBLE FORM IS RELEASED FROM RUPTURED CELLS BY THE ACTION OF A

CC PI-PLC.

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CC or send an email to license@isb-sib.ch).

DR EMBL; V01384; CAA24674.1; -;
DR PIR; S07329; S07329;
DR InterPro; IPR001812; Trypan glycop.
DR Pfam; PF00913; Trypan glycop; 1.
KW Glycoprotein; Antigen; Trypanosomiasis; GPI-anchor; Membrane; Signal.
FT SIGNAL 1 21 POTENTIAL
FT CHAIN 22 454 VARIANT SURFACE GLYCOPROTEIN ILRAT 1.BC.
FT PROPEP 455 471 HYDROPHOBIC, REMOVED DURING NATURATION.
FT CARBOHYD 130 130 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 454 454 GPI-ANCHOR.
SQ SEQUENCE 471 AA; 50520 MW; 3F31B229E295B6D1 CRC64;
Query Match 9.8%; Score 69.5; DB 1; Length 471;
Best Local Similarity 22.3%; Pred. No. 60;
Matches 23; Conservative 20; Mismatches 47; Indels 13; Gaps 3;
QY 2 ESTSTTNFVAENRPTGETFVDMREALLRVKSSERLMLRA-----LAGMCGHRVLP 54
Db 84 EQSTTSFLNSGSPTRRELTNQAIM--SQLEHIANEQYALLNVSATSTDTLD 141
QY 55 GTGASAIATAATVPKASM-----KLKPRPOSTKSPLELSRK 93
Db 142 GDGTQYNTGTSITSGFTVSKTTECNTEPSTEDTKPDQTLSKK 184

RESULT 40
SMC_BACSU STANDARD; PRT; 1186 AA.
AC P51834; O31735;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chromosome partition protein smc.
GN SMC.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1] SEQUENCE FROM N.A.
RP STRAIN=168;
RA Oguero A., Kakeshita H., Takamatsu H., Nakamura K., Yamane K.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2] SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borris R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holmappel S., Honono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasehara Y., Klearr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidis A., Lardinios S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowaka A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpsira P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viati A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis".
RL Nature 390:249-256(1997).
RN [3] SEQUENCE OF 1171-1186 FROM N.A.
RC STRAIN=168;
RX MEDLINE=96093930; PubMed=7584053;
RA Oguero A., Kakeshita H., Honda K., Takamatsu H., Nakamura K.,
RA Yamane K.;
RT "erb: a Bacillus subtilis gene encoding a homologue of the alpha-
RT subunit of the mammalian signal recognition particle receptor.";
RL DNA Res. 2:95-100(1995).
RN [4] CHARACTERIZATION.
RP MEDLINE=98367134; PubMed=9701812;
RX Moriya S., Tsujikawa E., Hassan A.K., Asai K., Kodama T.,
RA Ogasawara N.;
RT "A bacillus subtilis gene-encoding protein homologous to eukaryotic
RT SMC motor protein is necessary for chromosome partition.";
RL Mol. Microbiol. 29:179-187(1998).
RN [5] CHARACTERIZATION.
RP MEDLINE=98241483; PubMed=9573042;
RX Britton R.A., Lin D.C., Grossman A.D.;
RT "Characterization of a prokaryotic SMC protein involved in chromosome
RT partitioning.";
RL Genes Dev. 12:1254-1259(1998).
CC -!- FUNCTION: PLAYS AN IMPORTANT ROLE IN CHROMOSOME STRUCTURE AND
CC PARTITIONING. ESSENTIAL FOR CHROMOSOME PARTITION.
CC -!- SIMILARITY: BELONGS TO THE SMC FAMILY.
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DR EMBL; D64116; BAA10977.1; -;
DR EMBL; Z99112; CAB13467.1; -;
DR EMBL; D49781; BAA08615.1; -;
DR PIR; G69708; G69708.
DR Subtilist; BG11538; smc.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR003405; SMC_C.
DR InterPro; IPR003395; SMC_N.
DR Pfam; PF02483; SMC_C; 1.
DR ATP-binding; Coiled coil; Complete proteome.
FT NP BIND 31 38
FT DOMAIN 244 481 COILED COIL (POTENTIAL).
FT DOMAIN 664 943 COILED COIL (POTENTIAL).
FT DOMAIN 989 1031 COILED COIL (POTENTIAL).
FT CONFLICT 50 50 E -> G (IN REF. 1).
FT CONFLICT 162 162 E -> G (IN REF. 1).
FT CONFLICT 175 175 K -> E (IN REF. 1).
FT CONFLICT 178 178 E -> G (IN REF. 1).
FT CONFLICT 192 192 E -> G (IN REF. 1).
FT CONFLICT 228 228 A -> P (IN REF. 1).
FT CONFLICT 236 236 K -> E (IN REF. 1).
FT CONFLICT 254 254 A -> P (IN REF. 1).

FT CONFLICT 271 271 D -> G (IN REF. 1).
FT CONFLICT 284 284 N -> D (IN REF. 1).
FT CONFLICT 309 309 E -> D (IN REF. 1).
FT CONFLICT 336 342 KEELSKQ -> TERRAFA (IN REF. 1).
FT CONFLICT 365 365 Q -> H (IN REF. 1).
FT CONFLICT 438 438 E -> K (IN REF. 1).
FT CONFLICT 444 444 I -> P (IN REF. 1).
FT CONFLICT 475 475 A -> P (IN REF. 1).
FT CONFLICT 494 494 E -> D (IN REF. 1).
FT CONFLICT 515 515 E -> D (IN REF. 1).
FT CONFLICT 542 542 L -> V (IN REF. 1).
FT CONFLICT 546 546 A -> P (IN REF. 1).
FT CONFLICT 586 600 QSRDAETAARHSSFL -> SKPLRGSGPAPIISF (IN REF. 1).
FT CONFLICT 623 631 TVLITEDLK -> NRSDYRLKG (IN REF. 1).
FT CONFLICT 664 664 A -> S (IN REF. 1).
FT CONFLICT 676 676 S -> T (IN REF. 1).
FT CONFLICT 680 680 E -> G (IN REF. 1).
FT CONFLICT 694 694 A -> S (IN REF. 1).
FT CONFLICT 701 701 K -> Q (IN REF. 1).
FT CONFLICT 726 726 L -> V (IN REF. 1).
FT CONFLICT 738 740 LQV -> POF (IN REF. 1).
SQ SEQUENCE 1186 AA; 135510 MW; 0163227AAF2BCA2B CRC64;

Query Match 9.8%; Score 69.5; DB 1; Length 1186;
Best Local Similarity 26.0%; Pred.No. 1.8e+02;
Matches 39; Conservative 22; Mismatches 66; Indels 23; Gaps 7;

QY 2 ESTSTTNF--VAENRPTGETP-DVMREALLVKSSERLAMLRLAGMCGHR-----VLP 54
Db 591 ETARHSSFLGVASELVTFDDPAIRSVIQNLGTVLITEDLKANELAKLIGHRYRIVTLE 650

QY 55 G----TGASIAATVTPKGASMKLKPPRPOSTKSPELRELSRKIREMNK---TISQESAR 107
Db 651 GDVVNPGSGMTGGAVKKKNSL-----LGRSRELEDVTKLAEMEETALLEQEVKT 702

QY 108 VNHLPPEGHLEKRAEYFRHLRLSKSGV 137
Db 703 LKHSIQDMEXKLADLRETGEGLR-LKQQDV 731

Search completed: November 14, 2003, 10:39:23
Job time : 39 secs

OM protein - protein search, using sw model

Run on: November 14, 2003, 10:38:35 ; Search time 68 Seconds
(without alignments)
535.080 Million cell updates/sec

Title: US-10-087-573-2

Perfect score: 708

Sequence: 1 MESTSTTNFVAENRPTFGE.....RAEYFRHLRLSLKSGQVNRLLI 141

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 segs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_arChaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	708	100.0	141	5 Q8MN4	Q8mn4 babesia can
2	603	85.2	285	5 Q8MQH4	Q8mqh4 babesia can
3	87.5	12.4	610	13 Q91431	Q91431 xenopus lae
4	85	12.1	524	16 Q9YV10	Q9YV10 deinoxoccus
5	85	12.0	478	16 Q8PDC3	Q8pdc3 xanthomonas
6	84.5	11.9	609	13 Q92021	Q92021 xenopus lae
7	83	11.7	192	15 Q56002	Q56002 human immun
8	83	11.7	1053	4 Q95625	Q95625 homo sapien
9	82	11.6	192	15 Q55997	Q55997 human immun
10	82	11.6	192	15 Q78242	Q78242 human immun
11	82	11.6	192	15 Q56010	Q56010 human immun
12	82	11.6	192	15 Q56006	Q56006 human immun
13	82	11.6	239	16 Q8FVG5	Q8fyg5 anabaena sp
14	82	11.6	291	2 Q93T00	Q93tu0 acidithioba
15	82	11.6	988	10 P93661	P93661 chenopodium
16	81.5	11.5	378	11 Q8R089	Q8r089 mus musculus

17	81.5	11.5	1281	16 Q91211	Q91211 pseudomonas
18	81	11.4	192	15 Q55960	Q55960 human immun
19	81	11.4	192	15 Q56000	Q56000 human immun
20	81	11.4	192	15 Q56005	Q56005 human immun
21	81	11.4	192	15 Q79079	Q79079 human immun
22	80.5	11.4	412	4 Q8NHV2	Q8nhv2 homo sapien
23	80.5	11.4	448	4 Q8NA61	Q8na61 homo sapien
24	80.5	11.4	452	16 Q93IX7	Q93ix7 streptomyce
25	80.5	11.4	1157	5 Q3VP22	Q3vp22 drosophila
26	80.5	11.4	1157	5 Q8T9E1	Q8t9e1 drosophila
27	80	11.3	192	15 Q56008	Q56008 human immun
28	80	11.3	192	15 Q91QF2	Q91qf2 human immun
29	80	11.3	464	16 Q910T6	Q910t6 pseudomonas
30	80	11.3	819	13 Q9YHC1	Q9yhcl perca flave
31	80	11.3	895	13 Q9WGN1	Q9wgn1 perca flave
32	80	11.3	902	10 Q81209	Q81209 arabidopsis
33	80	11.3	902	10 Q8LY21	Q8ly21 arabidopsis
34	80	11.3	1017	2 Q8VW43	Q8vw43 bradyrhizob
35	79.5	11.2	211	5 Q9Y069	Q9y069 periplaneta
36	79.5	11.2	348	10 Q8VYQ4	Q8vyq4 arabidopsis
37	79.5	11.2	357	16 Q9RKL6	Q9rkl6 streptomyce
38	79.5	11.2	4065	3 Q9P421	Q9p421 neurospora
39	79	11.2	192	15 Q9YB41	Q9yb41 human immun
40	79	11.2	192	15 Q79093	Q79093 human immun
41	79	11.2	192	15 Q79105	Q79105 human immun
42	79	11.2	192	15 Q56009	Q56009 human immun
43	79	11.2	192	15 Q73459	Q73459 human immun
44	79	11.2	192	15 Q9WP97	Q9wp97 human immun
45	79	11.2	192	15 Q56004	Q56004 human immun

ALIGNMENTS

RESULT 1

Q8MN4

ID Q8MN4 PRELIMINARY; PRT; 141 AA.

AC Q8MN4

DT 01-OCT-2002 (TRENBLrel. 22, Created)

DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)

DE Putative vir15 protein.

GN VIR.

OS Babesia canis.

OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.

OX NCBI_TaxID=5867;

RN [1]

RP SEQUENCE FROM N.A.

RA Drakulovski P., Carcy B., Moubri K., Carret C., Depoix D.,

RA Schetters T.P.M., Gorenflot A.;

RT "An extrachromosomal dsRNA from Babesia canis implicated in parasite

RT virulence";

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ494862; CAD41951.1; --

SQ SEQUENCE 141 AA; 15752 MW; B84419C128FD7CD1 CRC64;

Query Match 100.0%; Score 708; DB 5; Length 141;
Best Local Similarity 100.0%; Pred. No. 2.5e-59;
Matches 141; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MESTSTTNFVAENRPTFGEFDVNR	REALLRVKSSERLAMLRALAGMCHRVLPCTGASA	60
DB	1	MESTSTTNFVAENRPTFGEFDVNR	REALLRVKSSERLAMLRALAGMCHRVLPCTGASA	60
QY	61	IAATVTPKGASMKLPPRPQSTKSP	ELSKIRKIREMNKTIQESARVNHRLPECHPLLE	120
DB	61	IAATVTPKGASMKLPPRPQSTKSP	ELSKIRKIREMNKTIQESARVNHRLPECHPLLE	120
QY	121	KRAEYFRHLRLSLKSGQVNRLLI	141	
DB	121	KRAEYFRHLRLSLKSGQVNRLLI	141	


```

RESULT 2
Q8MQH4 PRELIMINARY; PRT; 285 AA.
ID AC Q8MQH4;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Putative vir32 protein.
GN VIR.
OS Babesia canis.
OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
OX NCBI_TaxID=5867;
RN [1]
RP SEQUENCE FROM N.A.
RA Drakulovski P., Carcy B., Moubri K., Carret C., Depoix D.,
RA Schettler T.P.M., Gorenflot A.; Babesia canis implicated in parasite
RT "An extrachromosomal dsRNA from Babesia canis implicated in parasite
RL virulence."
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ494862; CAD41950.1;
SQ SEQUENCE 285 AA; 32169 MW; 45ACEFEC7927243D CRC64;

Query Match 85.2%; Score 603; DB 5; Length 285;
Best Local Similarity 90.4%; Pred. No. 5e-49;
Matches 122; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 MESTSTTNFVAENRPTFGTDFVMEALLRVKSSERLALAGVCGHRVLPGTGASA 60
DB 1 MESTSTTNFVAENRPTFGTDFVMEALLRVKSSERLALAGVCGHRVLPGTGASA 60
QY 61 IATVTPKGSMLKPPRPOSTKSPPELRSLKIRENMKTIISGARVNHRLPEGHPLLE 120
DB 61 IATVTPKGSMLKPPRPOSTKSPPELRSLKIRENMKTIISGARVNHRLPEGHPLLR 120
QY 121 KRAEYFRHLRLSLKSG 135
DB 121 SGQNIFVTLDLRAK 135

RESULT 3
Q91431 PRELIMINARY; PRT; 610 AA.
ID AC Q91431;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Nuclear factor 7.
GN XNF7-O.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Gong S.G., Reddy B.A., Etkin L.D.;
RA "Two forms of Xenopus nuclear factor 7 have overlapping spatial but
RT different temporal patterns of expression during development.";
RL Mech. Dev. 52:305-318(1995)
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: S80988; AAB35876.1;
DR InterPro: IPR001870; B302.
DR InterPro: IPR003649; Bbox.C.
DR InterPro: IPR000953; Chromo.
DR InterPro: IPR006574; PRY.
DR InterPro: IPR003877; SPRY.
DR InterPro: IPR003815; Znf_Box.
DR InterPro: IPR001841; Znf_Ring.
DR Pfam: PF00622; SPRY.1.
DR Pfam: PF00643; zf-B_box; 1.
DR Pfam: PF00097; zf-G3HC4; 1.
DR SMART; SMC0502; BBC; 1.

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DR SMART; SMC0336; BBOX; 1.
DR SMART; SMC0298; CHROMO; 1.
DR SMART; SMC0589; PRY; 1.
DR SMART; SMC0184; RING; 1.
DR SMART; SMC0449; SPRY; 1.
DR PROSITE; PS50119; ZF_BOX; 1.
DR PROSITE; PS00518; ZF_RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 610 AA; 69115 MW; D828F60060572EC1 CRC64;

Query Match 12.4%; Score 87.5; DB 13; Length 610;
Best Local Similarity 32.0%; Pred. No. 7.3;
Matches 31; Conservative 12; Mismatches 37; Indels 17; Gaps 4;

QY 50 HRVLP-----GTGASAIATVTPKGSMLKPPRPOSTKSPPELR-ELSRKIRENMKTIISQ 103
DB 256 HNFILPILDAIGVYRELSAIVAPLEASLKV-----TEQLSGEQSDKIEQHNNKVSQ 306
QY 104 ESARNVHRLPEGHPLLEKRAEYFRHLRLSLKSGQVNRLL 140
DB 307 YKEHTVTSFEKLHFLKEREE--KLLEQLKEQGDNLL 341

RESULT 4
Q9RY10 PRELIMINARY; PRT; 524 AA.
ID AC Q9RY10;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Protein kinase, putative.
GN DRA0332.
OS Deinococcus radiodurans.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Vamathevan J.J., Lam P., McDonald L.J., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus
RT radiodurans RI."
RL Science 286:1571-1577(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF001863; AAF12449.1;
DR TIGR; DRA0332;
DR InterPro: IPR000719; Prot_Kinase.
DR InterPro: IPR002965; P-rich_extensn.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00669; pkinase; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase;
KW Complete proteome.
SQ SEQUENCE 524 AA; 55298 MW; 79807356B6E2AED CRC64;

Query Match 12.1%; Score 86; DB 16; Length 524;
Best Local Similarity 29.0%; Pred. No. 8.5;
Matches 29; Conservative 23; Mismatches 28; Indels 20; Gaps 6;

QY 25 MREALL-----RVKSSERLALAGVCGHRVLPGTG-----ASAIATVTPKGSMLK 75

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Db 287 LREAVLSCHMAPRIENRQSA--QAL-----RRILRGEGTVTTAAPAAAPQPOQSPVR 339

Qy 76 P---PRQSTKSPBL-RELSRKIREMKNKTISQSARVNHR 111

Db 340 PSPAPTTPNPQTDREVEKRLRELEKEVRKEARQSR 379

RESULT 5

Q8PDC3 PRELIMINARY; PRT; 478 AA.

AC Q8PDC3;

DT 01-OCT-2002 (TReMBLrel. 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)

DE Hypothetical protein XCC0417.

GN XCC0417.

OS Xanthomonas campestris (pv. campestris).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=340;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33913 / NCPPB 528;

RX MEDLINE=2202145; PubMed=1204217;

RA da Silva A.C.R., Perro J.A., Reinach P.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Ciccarotte G., Cannavaro J., Cardoso J., Chamberg F., Ciapina L.P.,

RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locall E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Maidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.D., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Secubal J.C., Kitajima J.P.,

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

RT host specificities."

RL Nature 417:459-463(2002).

DR EMBL; AE012139; AAM39735.1; -

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 478 AA; 51984 MW; 9A239F7950580A89 CRC64;

Query Match 12.0%; Score 85; DB 16; Length 478;

Best Local Similarity 29.7%; Pred. No. 9.4;

Matches 27; Conservative 16; Mismatches 38; Indels 10; Gaps 3;

Qy 49 GHR----VLPGTASATAATVTPKGSMKLPKPPQSTKSPBLRELSRKIREMKNKTISQE 104

Db 216 GHRGLLAISRGGLAPQAHLRQP-GRALPPLQLQRAIKDADLRALRGVRLSVVDDW 274

Qy 105 SARVNHLRPEGHPL-----LEKRAEYFRHLR 130

Db 275 RRVDLALRPLQLWQRLSLSQARFLHLR 305

RESULT 6

Q92021 PRELIMINARY; PRT; 609 AA.

ID Q92021

AC Q92021;

DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)

DE XNF7=ZINC finger nuclear phosphoprotein.

GN XNF7.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92038424; PubMed=1936552;

RA Reddy B.A., Kloc M., Etkin L.;

RT "The cloning and characterization of a maternally expressed novel zinc

RT finger nuclear phosphoprotein (xnf7) in Xenopus laevis.";

RL Dev. Biol. 148:107-116(1991).

RN [2]

RP SEQUENCE FROM N.A.

RA Reddy B.A., Kloc M., Etkin L.D.;

RL Submitted (APR-1991) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL; S64515; AAB20269.1; -

DR EMBL; M63705; AAA49995.1; -

DR InterPro; IPR001870; B302.

DR InterPro; IPR000953; Chromo.

DR InterPro; IPR006574; PRY.

DR InterPro; IPR003877; SPRY receptor.

DR InterPro; IPR000315; Znf_Bbox.

DR InterPro; IPR001841; Znf_ring.

DR Pfam; PF00622; SPRY; 1.

DR Pfam; PF00643; Zf-B_box; 1.

DR Pfam; PF00097; Zf-C3HC4; 1.

DR SMART; SM00336; BBOX; 1.

DR SMART; SM00298; CHROMO; 1.

DR SMART; SM00589; PRY; 1.

DR SMART; SM00184; RING; 1.

DR SMART; SM00449; SPRY; 1.

DR PROSITE; PS00119; ZF_BBOX; 1.

DR PROSITE; PS00518; ZF_RING_1; 1.

DR PROSITE; PS00089; ZF_RING_2; 1.

KW Metal-binding; Zinc; Zinc-finger.

SQ SEQUENCE 609 AA; 68875 MW; 088C8312B45C78F8 CRC64;

Query Match 11.9%; Score 84.5; DB 13; Length 609;

Best Local Similarity 30.9%; Pred. No. 14;

Matches 30; Conservative 12; Mismatches 38; Indels 17; Gaps 4;

Qy 50 HRVLP-----GTGASATAATVTPKGSMKLPKPPQSTKSPBL-RELSRKIREMKNKTISQ 103

Db 255 HNFPLTDAVGVRBELSAVAPLEASLKV-----TEQLSSEQSDKIEOHKNMSQ 305

Qy 104 ESARVNHLRPEGHPLLEKRAEYFRHLRSLKSGQVNL 140

Db 306 YKEHITSEFKLHFLRREE--KULEQLKEQGENLL 340

RESULT 7

OS6002 PRELIMINARY; PRT; 192 AA.

ID OS6002

AC OS6002;

DT 01-JUN-1998 (TReMBLrel. 06, Created)

DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)

DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)

DE Vif protein (Virion infectivity factor) (SOR protein).

GN VIF.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EI08;

RX MEDLINE=98105749; PubMed=9445004;

RA Vedavalli V.R., Chappey C., Matala E., Ahmad N.;

RT "Conservation of an intact vif gene of human immunodeficiency virus

RT type 1 during maternal-fetal transmission.";

RL J. Virol. 72:1092-1102(1998).

CC -1- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).

DR EMBL; AF019511; AAC02385.1; -

DR InterPro; IPR000475; Viral_infect.

DR Pfam; PF00559; Vif; 1.

DR PRINTS; PR00349; VIRIONINFECT.

DR ProDom; PD000063; Viral_infect; 1.

```

KW AIDS.
SQ SEQUENCE 192 AA; 22545 MW; FE30C8963FF0E79 CRC64;
Query Match 11.7%; Score 83; DB 15; Length 192;
Best Local Similarity 28.8%; Pred. No. 4.8;
Matches 30; Conservative 10; Mismatches 32; Indels 32; Gaps 5;

QY 22 FDMVREALLRVKSSERLAMLRLAG-----MCGHRVLPGTGASAIATVTPKGASM 72
DB 112 FDCFSASAIR-----KALLGHRVSPRCNYQAGHNQSLQYKALAALIKPK----- 157
QY 73 KLKPPRPQSTKPELRLSKIRKEMNKTIQSASRVNHLRPEGH 116
DB 158 KIKPPLPSVTKLTEDR-----WNKPQTKGHRGNHTM-DGH 192

RESULT 8
O95625 PRELIMINARY; PRT; 1053 AA.
ID O95625
AC O95625;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Zinc finger protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tang C.M., Seto E.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
EMBL; U69274; AAD00172.1; -.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF00651; BTB_1.
DR Pfam; PF00096; zf-C2H2; 12.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00355; Znf_C2H2; 12.
DR PROSITE; PS50097; BTB; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 12.
DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 12.
KW Metal-binding; Zinc; Zinc-finger.
SQ SEQUENCE 1053 AA; 119382 MW; C7B3C518534BF2D6 CRC64;

Query Match 11.7%; Score 83; DB 4; Length 1053;
Best Local Similarity 25.4%; Pred. No. 38;
Matches 34; Conservative 18; Mismatches 66; Indels 16; Gaps 5;

QY 9 NFVAENRPY-FGETFDVMEALLRVKSSERLAMLRLAGM---CGHRVLPGTGASAIIA 63
DB 486 NLVASTAKTNFGDDDTYR-SRLQRSVNEGAVIRLHKGEKQLQRKAVPKSAVOOVAQ 544
QY 64 TVTPKGASKMLKPPRPQSTKPELRLSKIRKEMNKTIQSASRVNHLRPEGH-----P 117
DB 545 KLVQRGKKVK---QPKRDAKENTEEASHKCGCGMVFORYVALIMHLKGERDYKCP 600
QY 118 LLEKRAEYFRHLRS 131
DB 601 LCKKQFQYSASLRA 614

RESULT 9
O55997 PRELIMINARY; PRT; 192 AA.
ID O55997
AC O55997;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Varion infectivity factor) (SOR protein).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

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RT "Conservation of an intact vif gene of human immunodeficiency virus
type 1 during maternal-fetal transmission.";
RL J. Virol. 72:1092-1102(1998).
CC -|- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
DR EMBL; AF019515; AAC02389.1; -
DR InterPro; IPR000475; Viral_infect.
DR Pfam; PF00559; Vif; 1
DR PRINTS; PR00349; VIRIONINFECT.
DR ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22572 MW; FD01CC08B5E4B0BD CRC64;

Query Match 11.6%; Score 82; DB 15; Length 192;
Best Local Similarity 28.0%; Pred.No. 6;
Matches 30; Conservative 9; Mismatches 30; Indels 38; Gaps 5;

QY 22 FQVNRALLRVKSSERLAMLALAGVCGHRVLEGTGAS-----AIATVTPKG 69
DB 112 FDCFSSEAIR-----KALLGHRVSPRCVYQAGHNKVGSLQYLALALIKPK- 157

QY 70 ASMKLPPRPQSTKSPELRELSRKIREMKNKTIQSARVNHRLPEGH 116
DB 158 ---KIRPPLPSVTKLTEDR-----WNKPQTKGHRGNHTW-DGH 192

RESULT 13
Q8YVG5 PRELIMINARY; PRT; 239 AA.
ID Q8YVG5
AC Q8YVG5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein All2013.
OS ALL2013.
GN Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003587; BAB73712.1; -
DR InterPro; IPR001601; Methyltransf.
DR InterPro; IPR000051; SAM bind.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 239 AA; 26707 MW; 71345D5EC7FDEB66 CRC64;

Query Match 11.6%; Score 82; DB 16; Length 239;
Best Local Similarity 26.9%; Pred.No. 7.8;
Matches 21; Conservative 16; Mismatches 39; Indels 2; Gaps 1;

QY 61 IAATVTPKGASMKLPPRPQSTKSPELRELSRK--IREMKNKTIQSARVNHRLPEGHPL 118
DB 141 IAASLTTPGCFWNADPILPESPTLAEIYQAAREWVSEQGSNFTVRKVGDSPPQYSN 200

QY 119 LEKRAEYFRHLRLSKSQ 136
DB 201 PQCLATLDTLQMLTKSG 218

RESULT 14
Q93TU0 PRELIMINARY; PRT; 291 AA.
ID Q93TU0
AC Q93TU0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

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DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Helicase-like protein.
GN REPA.
OS Acidithiobacillus caldus.
OG Plasmid pTC-F14.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Acidithiobacillus.
OX NCBI_TaxID=33059;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2124728; PubMed=11344137;
RT Gardner M.N.; Deane S.M.; Rawlings D.E.;
RA "Isolation of a New Broad-Host-Range IncQ-Like Plasmid, pTC-F14, from
RT the Acidophilic Bacterium Acidithiobacillus caldus and Analysis of the
RT Plasmid Replicon."
RL J. Bacteriol. 183:3303-3309(2001).
RW EMBL; AF325537; AAK56915.1; -.
KW Plasmid
SQ SEQUENCE 291 AA; 31324 MW; D8726E4864C7609B CRC64;

Query Match 11.6%; Score 82; DB 2; Length 291;
Best Local Similarity 23.4%; Pred.No. 9.9;
Matches 33; Conservative 28; Mismatches 56; Indels 24; Gaps 5;

QY 11 VAEN---RPTFGTFTDVMEALRVKSSERLAMLRLALA-----GNCGH--- 50
DB 101 IAEVLTLPTGKELNIMDEAHLRHRIIEASGARLIVDTLSRIHNUDENSNGMAHLVA 160
QY 51 ---RVLPGTGASIAAATVTPKSGASKMLKPPRPOSTK-SPBELRLSRKIRENMKTIQSESA 106
DB 161 TLEHIAASTGASVLYLHHVSGKSGMAGQTDQQAARGASALIDNARWCGYVAKVAEHA 220
QY 107 RVNHLRPEGHPLLEKRAEYFR 127
DB 221 RLSDRSFDRAPIGDRRGFFVR 241

RESULT 15
P93661 PRELIMINARY; PRT; 988 AA.
AC P93661;
DT 01-MAY-1997 (T-EMBLrel. 03, Created)
DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
DE Mitochondrial single-subunit DNA-dependent RNA polymerase.
OS Chenopodium album (lamb's-quarters).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Chenopodium.
NCBI_TaxID=3559;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97315321; PubMed=9171081;
RA Weihe A., Hedtke B., Boerner T.;
RT "Cloning and characterization of a cDNA encoding a bacteriophage-type
RT RNA polymerase from the higher plant Chenopodium album."
RL Nucleic Acids Res. 25:2319-2325(1997).
RW EMBL; Y08067; CAA69305.1; -.
DR HSSP; P00573; IARO.
DR InterPro; IPR002092; RNA_pol_phase.
DR Pfam; PF00940; RNA_pol_1.
DR PROSITE; PS00900; RNA_POL_PHAGE_1; 1.
DR PROSITE; PS00489; RNA_POL_PHAGE_2; 1.
SQ SEQUENCE 988 AA; 111854 MW; 65B5496C425D31A9 CRC64;

Query Match 11.6%; Score 82; DB 10; Length 988;
Best Local Similarity 25.9%; Pred.No. 44;
Matches 29; Conservative 17; Mismatches 52; Indels 14; Gaps 3;

QY 11 VAENRPTFGTFTDVMEALRVKSSERLAMLRLALACMGCHRVLPGTGASIAAATVTPKGA 70
DB 216 VGENRPLYGCTDFELPADMAVITMKLMGLL-----MTG-----SGNGGTTVQAATQIGE 267

QY 71 SKMLKPPRPOSTKSPBELRLSRKIRENMKTIQSESARVNHLRPEGHPLLEKR 122

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[illegible]

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RESULT 18
OS5960
ID O55960 PRELIMINARY; PRT; 192 AA.
AC O55960;
DT 01-JUN-1998 (TtEMBLrel. 06, Created)
DT 01-JUN-1998 (TtEMBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TtEMBLrel. 22, Last annotation update)
DE Vif protein (Vifon infectivity factor) (SOR protein).
VIF.
GN GN
OS Human immunodeficiency virus 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.

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RA VEDAVALLI V.R., CHAPPEY C., MATALE E., AHMAD N.;
RT "Conservation of an intact vif gene of human immunodeficiency virus
RT type 1 during maternal-fetal transmission.";
J. Virol. 72:1092-1102(1998).
R L.
- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
DR EMBL; AF019458; AAC02338.1; -.
DR InterPro; IPR000475; Viral_infect.
DR Pfam; PF00559; Vif; 1.
DR PRINTS; PR00349; VIRIONINFECT.
DR ProDom; PD000063; Viral_infect; 1.
DR AIDS.
SQ SEQUENCE 192 AA; 22410 MW; D841DA0216CC54AB CRC64;

Query Watch 11.4%; Score 81; DB 15; Length 192;
Best Local Similarity 27.8%; Pred. No. 7.4;
Matches 29; Conservative 12; Mismatches 32; Indels 32; Gaps 5;

QY 21 TFDWMEALLRVKSSERLAMELAG-----MCHRVLPETGASATAATVTPKGS 71
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 111 SFDCESESAR-----NAILGRIVPSCDFQAGHNKVGSLQVLAAALITPK--- 157
: : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 72 MKLKPPRPOSTKPELRELSRKIRENNKTKISQESARVNHRLPEGH 116
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 158 -KIKPLPSPVAKUTEDR-----WNKPQKTGSRGSRHM-NGH 192
: : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT	PRELIMINARY	PTT	192 AA
OS6000			
ID	OS6000		
AC	AC		
DT	01-JUN-1998	(T=EMBLrel. 06, Created)	
DT	01-JUN-1998	(T=EMBLrel. 06, Last sequence update)	
DT	01-OCT-2002	(T=EMBLrel. 22, Last annotation update)	
DE	Vif protein (Viron infectivity factor) (SOR protein).		
GN	Vif.		
OS	Human immunodeficiency virus 1.		
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.		
OX	NCBI_TaxId=11676;		
1]	RN		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=EI06;		
RX	MEDLINE=98105749; PubMed=9445004;		
RA	Yedavalli V.R., Chappey C., Matala E., Ahmad N.;		

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RT "Conservation of an intact vif gene of human immunodeficiency virus
RT type 1 during maternal-fetal transmission.";
RT J. Virol. 72:1092-1102(1998).
CC -1- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
DR EMBL; AF019509; AAC02383.1; -.
DR InterPro; IPR000475; Viral_infect.
DR Pfam; PF00559; Vif; 1.
DR PRINTS; PR00349; VIRIONINFFCT.
DR ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22473 MW; 707084D505264482 CRC64;

Query Match 11.4%; Score 81; DB 15; Length 192;
Best Local Similarity 28.0%; Pred. No. 7.4;
Matches 30; Conservative 8; Mismatches 31; Indels 38; Gaps 5;

Qy 22 FDMVREALURVKSSSLAMLRALAGCGHRVLPGTGAS-----AIAATVTPKG 69
Db 112 FDCFSSEAIR-----:|||||:|||||:|||||:|||||:|||||
Qy 70 ASMKLAPPSPQSTKSPELRELSRKIREMNKTIQSBSARVNNHRLPEGH 116
Db 158 ---KIRAPLPSTVKLTEDR-----WNKPKTKGHRGNHTM-NGH 192

RESULT 20
O56005 PRELIMINARY; PRT; 192 AA.
AC O56005;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Viron infectivity factor) (SOR protein).
OS VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=E111;
RX MEDLINE=98105749; PubMed=9445004;
RA Vedavalli V.R., Chappey C., Marala E., Ahmad N.;
RT "Conservation of an intact vif gene of human immunodeficiency virus
RT type 1 during maternal-fetal transmission.";
RT J. Virol. 72:1092-1102(1998).
CC -1- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
DR EMBL; AF019514; AAC02388.1; -.
DR InterPro; IPR000475; Viral_infect.
DR Pfam; PF00559; Vif; 1.
DR PRINTS; PR00349; VIRIONINFFCT.
DR ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22428 MW; 62F54F070104CDE7 CRC64;

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Best Local Similarity 28.0%; Pred.No. 7.4;
Matches 30; Conservative 8; Mismatches 31; Indels 38; Gaps 5;

QY 22 FDVMEALLRVKSSERLAMLRALAGMCGRVLPQGTGAS-----ATAATVTPKG 69
Db 112 FDFSESAR-----QALLGHRVSPRCDAQHNKVGSLQYLALALIKPK- 157

QY 70 ASWKUKPPRPQSTKSEURELSRKIRENMNTISQBSARVNHRLPEGH 116
Db 158 ---KIKPPLPSVTKLTEDR-----WNKPQTKGHRGNHTM-NGH 192

RESULT 21
Q79079
ID Q79079 PRELIMINARY; PRT; 192 AA.
AC Q79079;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DT Vif (viral infectivity factor) (Viron infectivity factor) (SOR
 DE protein).
 GN Vif.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94303241; PubMed=8030283;
 RA Wieland U., Hartmann J., Suhr H., Salzberger B., Eggers HJ.,
 RA Kuehn J.E.;
 RT "In vivo genetic variability of the HIV-1 vif gene."
 RL Virology 203:43-51(1994).
 CC -!- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
 DR EMBL; Z30687; CA83167.1;
 DR InterPro; IPR000475; Viral_infect.
 DR Pfam; PF00559; Vif; 1
 DR PRINTS; PR00349; VIRIONINFECT.
 DR PRODOM; PD000063; Viral_infect; 1.
 KW AIDS.
 SQ SEQUENCE 192 AA; 22529 MW; 20CD70E9953B8DCC CRC64;
 Query Match 11.4%; Score 81; DB 15; Length 192;
 Best Local Similarity 29.8%; Pred. No. 7.4;
 Matches 31; Conservative 8; Mismatches 33; Indels 32; Gaps 5;
 Qy 22 PDVREALLRVKSSERLALALAG-----MCHRVLPGTGASAIATVTPKGASM 72
 Db 112 FDCSESAIR-----KAILGHIVSPCEYQAGHNVKVSQYLALALVTPK--- 157
 Qy 73 KLKPPRQSTKSPELRELSRKIREMNKTIQESARVNHRLPEGH 116
 Db 158 KTKPLPSVTKLTEDR-----WNKPKQTKGRENHTM--NGH 192

RESULT 22
 Q8NHV2
 ID Q8NHV2 PRELIMINARY; PRT; 412 AA.
 AC Q8NHV2;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Similar to RIKEN CDNA 1700086N05 gene.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Strausberg R.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC027609; AAH27609.1;
 SQ SEQUENCE 412 AA; 47288 MW; 6EC3B47EF08CDE10 CRC64;
 Query Match 11.4%; Score 80.5; DB 4; Length 412;
 Best Local Similarity 29.8%; Pred. No. 21;
 Matches 28; Conservative 15; Mismatches 42; Indels 9; Gaps 3;
 Qy 48 CGHRVLPGTGASAIATVTPKGASMKLPPRPQSTKSPELRELSRKIREMNKTIQESAR 107
 Db 256 CSPGLQDQSGLSRPEEPKG-----PPARQE-DSKELRALRKVMNSGSGSEBEAK 308
 Qy 108 VNHRLPGHPLLEKRAEYFRHLRSLSKSGVNRLL 141
 Db 309 VGPGLPDGCQPLQLLRMRQALQALLKE--NRLL 340

RESULT 23
 Q8NA61
 ID Q8NA61 PRELIMINARY; PRT; 448 AA.
 AC Q8NA61;

01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein FLJ35810.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Oshima A., Takahashi-Fujii A., Tanase T., Inose N., Takeuchi K.,
 RA Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
 RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
 RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
 RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
 RA Sugakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
 RA Surano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK093129; BAC04067.1;
 KW Hypothetical protein.
 SQ SEQUENCE 448 AA; 51570 MW; D59271CFE59F8863 CRC64;
 Query Match 11.4%; Score 80.5; DB 4; Length 448;
 Best Local Similarity 29.8%; Pred. No. 23;
 Matches 28; Conservative 15; Mismatches 42; Indels 9; Gaps 3;
 Qy 48 CGHRVLPGTGASAIATVTPKGASMKLPPRPQSTKSPELRELSRKIREMNKTIQESAR 107
 Db 292 CSPGLQDQSGLSRPEEPKG-----PPARQE-DSKELRALRKVMNSGSGSEBEAK 344
 Qy 108 VNHRLPGHPLLEKRAEYFRHLRSLSKSGVNRLL 141
 Db 345 VGPGLPDGCQPLQLLRMRQALQALLKE--NRLL 376

RESULT 24
 Q93IX7
 ID Q93IX7 PRELIMINARY; PRT; 452 AA.
 AC Q93IX7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein SC01293.
 GN SC01293 OR SCBAC36F5.04.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Saunders D., Harris D.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RA Cerdano A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2);
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RL the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=21996410; PubMed=12000953;

RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Lark L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietsorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RL coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR ENBL; AL639108; CAC42840.1; -;
DR InterPro; IPR000182; ACT.
DR InterPro; IPR000182; GNSacetyltransf.
DR Pfam; PF00583; ACTyltransf; 1.
DR Pfam; PF01842; ACT; 1.
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 452 AA; 47341 MW; 1EBAFA60318FCD21 CRC64;
Query Match 11.4%; Score 80.5; DB 16; Length 452;
Best Local Similarity 32.3%; Pred. No. 23;
Matches 31; Conservative 12; Mismatches 28; Indels 25; Gaps 5;
OY 41 LRALAGMCHRVLP-----GTGASAIATVTPKGA-----SMKLKPP-----RPOSTK 83
DB 192 LRQLLGRCTIRSLPAPADDGAGAA-AAVPPGALGLEDTLRLURAPGGVSVRPHLPF 250
OY 84 SPEURELSKIRENMKNTSIESARVNHRLPEGHPL 119
DB 251 TPAEFARALVELD-----ASLGRVPRGRDVL 279
RESULT 25
Q9VP22 PRELIMINARY; PRT; 1157 AA.
ID Q9VP22 PRELIMINARY; PRT; 1157 AA.
AC Q9VP22 PRELIMINARY; PRT; 1157 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CG7597 protein.
GN CG7597.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10711132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Baer A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherris J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li Z., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reihert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Stimpson M., Stimpson M., Smith T.,
RA Spier E., Sridharan R., Turner C., Turner R., Venter E., Wang A.H., Wang X.,
RA Switzkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J.J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AE003594; AAF51738.1; -;
DR HSSP; P24941; LHCL.
DR FlyBase; FBgn0037093; CG7597.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_Kinase; 1.
DR SMART; SM00220; S_TKc_1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1157 AA; 128332 MW; B37ADCFBAC4E9F3 CRC64;
Query Match 11.4%; Score 80.5; DB 5; Length 1157;
Best Local Similarity 28.4%; Pred. No. 73;
Matches 25; Conservative 13; Mismatches 37; Indels 13; Gaps 3;
OY 55 GTGASAIATVTPKGA--MKLKPPR-----QSTKSPFELSLR--KIRENMKTI 101
DB 462 GTGTGDRYSRPTSSRYMSSPPVSGASGSHYHRRSPRMQRTRGDSRRSPSSA 521
OY 102 SCSARVNHRLPEGHPLLEKRAEYFRHL 129
DB 522 SSSASRSRSPSTRDLKHKREYINKI 549
RESULT 26
Q8T9E1 PRELIMINARY; PRT; 1157 AA.
AC Q8T9E1 PRELIMINARY; PRT; 1157 AA.
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SD04681p.
GN CG7597.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AY069806; AAL3951.1; -;
DR HSSP; P24941; 1BUH.
DR FlyBase; FBgn0037093; CG7597.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.


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DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
DR PROSITE; PS00107; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1157 AA; 128361 MW; ED0A30B3D9B5C786 CRC64;

Query Match 11.4%; Score 80.5; DB 5; Length 1157;
Best Local Similarity 28.4%; Pred.No.73;
Matches 25; Conservative 13; Mismatches 37; Indels 13; Gaps 3;

QY 55 GTGASAIATVTPKGAS-MKLKPPRP-----QSTKSPELRELSR-KIREMKNKI 101
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 462 GTCTGDSGRSRSPTSRYSRVESPPSPVGSAGSHYHRRSPMRQRTGDSRRSRPSSA 521
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 102 SQSARVNHRLPEGHDLLEKEAYFRHL 129
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 522 SSSASRSRSPTSRDLKHKREYIINKI 549
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 27
OS5008 PRELIMINARY; PRT; 192 AA.
ID ID 056008 PRELIMINARY; PRT; 192 AA.
OS 056008;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Vifon infectivity factor) (SOR protein).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=EM02;
RX MEDLINE=98105749; PubMed=9445004;
RA Yedavalli V.R., Chappay C., Matala E., Ahmad N.;
RT "Conservation of an intact vif gene of human immunodeficiency virus
RT type 1 during maternal-fetal transmission.";
RL J. Virol. 72:1092-1102(1998).
CC -I- FUNCTION: DETERMINES VIRUS INFECTIVITY (BY SIMILARITY).
DR ENEL; AF019518; AAC02391.1;-.
DR InterPro; IPR000475; Viral_infect.
DR Pfam; PF00559; Vif; 1.
DR PRINTS; PR00349; VIRIONINFCT.
DR ProDom; PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22587 MW; 39257817A1934935 CRC64;

Query Match 11.3%; Score 80; DB 15; Length 192;
Best Local Similarity 28.8%; Pred.No.9.2; 33; Indels 32; Gaps 5;
Matches 30; Conservative 9; Mismatches 9;

QY 22 FDMREALLRVKSGSERLAMLRLALAG-----MCGHRVLPGTGASAIATVTPKGASM 72
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 112 FDCFSESAIR-----KALLGHRVSPRRDYQAGNHVGSLOYLALALIKPKG--- 158
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 73 KLKPPRQSTKSPELRELSKIREMKNKTSQESARVNHRLPEGH 116
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 159 -IRPPLFSVTKLIEDR-----WNKPQTKGHRGNHTW-NGH 192
    ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 28
Q9IQF2 PRELIMINARY; PRT; 192 AA.
ID ID Q9IQF2 PRELIMINARY; PRT; 192 AA.
OS Q9IQF2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Vif protein (Vifon infectivity factor) (SOR protein).
GN VIF.
OS Human immunodeficiency virus 1.

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QY 76 -PFRQSTKSPELRLSKIREMKNKTIQESARVNHRLPEGHPLLEKRA-----EYF 126
 DB 337 IAPRPQ--MPAEYRKLAEQARRLT-----VNFREFQSALLDNKALLDQVRLLDYL 385
 QY 127 RHLRLSKSGV 137
 DB 386 RQNRKLQERTV 396
 RESULT 30
 Q9YHCL1 PRELIMINARY; PRT; 819 AA.
 AC Q9YHCL1;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Lysyl oxidase-like protein (Fragment).
 GN PLO1.
 OS Perca flavescens (Yellow perch).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 OC Percidae; Perca.
 OX NCBI_TaxID=8167;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Langenau D.M., Goetz F.W., Roberts S.B.;
 RT "Progestin-upregulated mRNAs in the yellow perch ovary."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF103901; AAC79085.2; -
 DR InterPro; IPR001695; Lysyl oxidase.
 DR InterPro; IPR001190; Srcr receptor.
 DR Pfam; PF01186; Lysyl oxidase; 1.
 DR Pfam; PF00530; SRCR; 4.
 DR PRINTS; PR00074; LYSILOXIDASE.
 DR PRODOM; PD013887; SPERACTRCPT. 1.
 DR SMART; SM00202; SR; 4.
 DR PROSITE; PS00420; SRCR 1; 1.
 DR PROSITE; PS50287; SRCR 2; 4.
 FT NON_TER 1 1
 SQ SEQUENCE 819 AA; 91379 MW; 47B9215FA942B119 CRC64;
 Query Match 11.3%; Score 80; DB 13; Length 819;
 Best Local Similarity 23.7%; Pred. No. 54;
 Matches 28; Conservative 14; Mismatches 42; Indels 34; Gaps 2;
 QY 44 LAGMCHRVLPGTGASAI-----AATVTPKGASMKLKPPOSTK----- 83
 DB 49 LGVICSPERRPGSPAVAVEAEAPSSSRHQPNQPGORPPPLPQSVPPPAHISSSSARGHEI 108
 QY 84 -----SPELRLSKIREMKNKTIQESARVNHRLPEGHPLLEKRAYFR 127
 DB 109 ALHRNPTSSRRSIISPOENGHEIQILRRNRGSSRASQVNPALPQGHQLLSRLANGYR 166
 RESULT 31
 Q9W6N1 PRELIMINARY; PRT; 895 AA.
 AC Q9W6N1;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 20, Last annotation update)
 DE Lysyl oxidase related protein homolog.
 GN FLO2.
 OS Perca flavescens (Yellow perch).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
 OC Percidae; Perca.
 OX NCBI_TaxID=8167;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Langenau D.M., Goetz F.W., Roberts S.B.;
 RT "Progestin-upregulated mRNAs in the yellow perch ovary."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF103901; AAC79085.2; -
 DR InterPro; IPR001695; Lysyl oxidase.
 DR InterPro; IPR001190; Srcr receptor.
 DR Pfam; PF01186; Lysyl oxidase; 1.
 DR Pfam; PF00530; SRCR; 4.
 DR PRINTS; PR00074; LYSILOXIDASE.
 DR PRODOM; PD013887; SPERACTRCPT. 1.
 DR SMART; SM00202; SR; 4.
 DR PROSITE; PS00420; SRCR 1; 1.
 DR PROSITE; PS50287; SRCR 2; 4.
 FT NON_TER 1 1
 SQ SEQUENCE 819 AA; 91379 MW; 47B9215FA942B119 CRC64;
 Query Match 11.3%; Score 80; DB 13; Length 819;
 Best Local Similarity 23.7%; Pred. No. 54;
 Matches 28; Conservative 14; Mismatches 42; Indels 34; Gaps 2;
 QY 44 LAGMCHRVLPGTGASAI-----AATVTPKGASMKLKPPOSTK----- 83
 DB 49 LGVICSPERRPGSPAVAVEAEAPSSSRHQPNQPGORPPPLPQSVPPPAHISSSSARGHEI 108
 QY 84 -----SPELRLSKIREMKNKTIQESARVNHRLPEGHPLLEKRAYFR 127
 DB 109 ALHRNPTSSRRSIISPOENGHEIQILRRNRGSSRASQVNPALPQGHQLLSRLANGYR 166

RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX Langenau D.M., Goetz F.W., Roberts S.B.;
 RA "The upregulation of messenger ribonucleic acids during 17alpha,
 RT 20beta-dihydroxy-4-pregnen-3-one-induced ovulation in the perch
 RT ovary";
 RL J. Mol. Endocrinol. 23:137-152(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RA Roberts S.B., Goetz F.W.;
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF143003; AAD33900.1; -
 DR InterPro; IPR001695; Lysyl oxidase.
 DR InterPro; IPR001190; Srcr receptor.
 DR Pfam; PF01186; Lysyl oxidase; 1.
 DR Pfam; PF00530; SRCR; 4.
 DR PRINTS; PR00074; LYSILOXIDASE.
 DR PRODOM; PD013887; SPERACTRCPT. 1.
 DR SMART; SM00202; SR; 4.
 DR PROSITE; PS00420; SRCR 1; 1.
 DR PROSITE; PS50287; SRCR 2; 4.
 SQ SEQUENCE 895 AA; 99621 MW; E18627D1604896B7 CRC64;
 Query Match 11.3%; Score 80; DB 13; Length 895;
 Best Local Similarity 23.7%; Pred. No. 50;
 Matches 28; Conservative 14; Mismatches 42; Indels 34; Gaps 2;
 QY 44 LAGMCHRVLPGTGASAI-----AATVTPKGASMKLKPPOSTK----- 83
 DB 125 LGVICSPERRPGSPAVAVEAEAPSSSRHQPNQPGORPPPLPQSVPPPAHISSSSARGHEI 184
 QY 84 -----SPELRLSKIREMKNKTIQESARVNHRLPEGHPLLEKRAYFR 127
 DB 185 ALHRNPTSSRRSIISPOENGHEIQILRRNRGSSRASQVNPALPQGHQLLSRLANGYR 242
 RESULT 32
 O81209 PRELIMINARY; PRT; 902 AA.
 AC O81209;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Respiratory burst oxidase protein A.
 GN RBOHA.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucotsids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Landsberg erecta;
 RX MEDLINE=98291500; PubMed=9628030;
 RA Torres M.A., Onouchi H., Hamada S., Machida C.h., Hammond-Kosack K.E.,
 RA Jones J.D.G.;
 RT "Six Arabidopsis thaliana homologues of the human respiratory burst
 RT oxidase (gp91phox).";
 RL Plant J. 14:365-370(1998).
 DR EMBL; AF055353; AAC39475.1; -
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR002916; Ferric_reduct.
 DR InterPro; IPR000778; GP91PHOX.
 DR Pfam; PF00036; ehand; 1.
 DR Pfam; PF01794; Ferric_reduct; 1.
 DR PRINTS; PR00466; GP91PHOX.
 DR PROSITE; PS00018; EF_HAND; 1.
 SQ SEQUENCE 902 AA; 102996 MW; 02B9B8A97DEFB318 CRC64;
 Query Match 11.3%; Score 80; DB 10; Length 902;

Best Local Similarity 25.2%; Pred. No. 60;
Matches 37; Conservative 22; Mismatches 42; Indels 46; Gaps 7;
QY 3 STSTTNFVAENRPTGTFDVT-----MREALRV-KSERLA 39
Db 31 NVATTSNYGEDEPYVEITLDIHDDSVVGLKSPNHRGAGSNYEDQSLLRQGRSGRNS 90
QY 40 MLRALAGMCHRVLPGTGASAIATVTPKGSMKLPKPPRQSTK---SPELRELSRK-IR 95
Db 91 VLKRLASSV-----STGITRVASSVSSSAR---KPPRQLAKLRRSKRAELALKGLK 141
QY 96 EMNKTISQESARVNHRLPEGHPLLEKR 122
Db 142 FITKTDG-----VTGWPEVEKR 158
RESULT 33
Q9LY21 PRELIMINARY; PRT; 902 AA.
AC Q9LY21
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Respiratory burst oxidase protein A.
GN T211.100.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosidea II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Rudd S., Lemcke K., Mayer K.F.X.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL163912; CAB87928.1; .
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR002916; Ferric_reduct.
DR InterPro; IPR000778; GP91Phox.
DR Pfam; PF00036; eifhand; 1.
DR Pfam; PF01794; Ferric_reduct; 1.
DR PRINTS; PR00466; GP91PHOX.
DR PROSITE; PS00018; EF HAND; 1.
SQ SEQUENCE 902 AA; 102935 MW; E43286CAD4F857B2 CRC64;
Query Match 11.3%; Score 80; DB 10; Length 902;
Best Local Similarity 25.2%; Pred. No. 60;
Matches 37; Conservative 22; Mismatches 42; Indels 46; Gaps 7;
QY 3 STSTTNFVAENRPTGTFDVT-----MREALRV-KSERLA 39
Db 31 NVATTSNYGEDEPYVEITLDIHDDSVVGLKSPNHRGAGSNYEDQSLLRQGRSGRNS 90
QY 40 MLRALAGMCHRVLPGTGASAIATVTPKGSMKLPKPPRQSTK---SPELRELSRK-IR 95
Db 91 VLKRLASSV-----STGITRVASSVSSSAR---KPPRQLAKLRRSKRAELALKGLK 141
QY 96 EMNKTISQESARVNHRLPEGHPLLEKR 122
Db 142 FITKTDG-----VTGWPEVEKR 158
RESULT 34
Q8VM43 PRELIMINARY; PRT; 1017 AA.
ID Q8VM43
AC Q8VM43
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

Proline dehydrogenase.
GN PUTA.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GX201;
RA Wu B., Tang X., Bai X., Tang D., Lu A., Tang J., Ma O.;
RT "Bradyrhizobium japonicum strain GX201 proline dehydrogenase gene
putA";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
DR EMBL; AF306633; AAL35755.1; .
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR002872; Pro dh.
DR InterPro; IPR001560; WD40.
DR Pfam; PF00171; aldehyd; 1.
DR Pfam; PF01619; Pro dh; 1.
DR PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
KW Oxidoreductase.
SQ SEQUENCE 1017 AA; 111472 MW; E4B350B0B4E5A5B CRC64;
Query Match 11.3%; Score 80; DB 2; Length 1017;
Best Local Similarity 18.8%; Pred. No. 70;
Matches 38; Conservative 28; Mismatches 50; Indels 86; Gaps 7;
QY 5 STTNFVAENRPTGTFDVTMREALRVKSSERLAMLRLAGMC-----GHRV 52
Db 585 SRSAHFIALLOPEGGKTLD-----DALSDLREADFERYAAQGRKLPASETA 632
QY 53 LPGTGASAIATVTPKGSMKLP-----PRQS----- 81
Db 633 MFGNGESNALTMRGGAFAISPMNFFLAIFLQGVTAALMAGNVVAKPAEQTPRIARG 692
QY 82 -----TKSPELRELSRKIRMNKTIQSARVN-----HRLPEGHPLLEKRAEYFRHLRS 131
D., 693 RSPAARSRHQPQEAASRRHRPHRRRADBSHRRRLRLDRGRP-----QHQT 743
QY 132 LKSQ-----GVNRLI 141
Db 744 LAAKDGRIVPLIAETGGINAMI 765
RESULT 35
Q9Y069 PRELIMINARY; PRT; 211 AA.
ID Q9Y069
AC Q9Y069
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative transcription factor.
GN PA-EN2.A.
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=21110537; PubMed=11180849;
RA Marie B., Bacon J.P.;
RT "Two engrailed-related genes in the cockroach: cloning, phylogenetic
analysis, expression and isolation of spliced variants";
RL Dev. Genes Evol. 210:436-448(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=20180522; PubMed=10712910;
RA Marie B., Bacon J.P., Blagburn J.M.;

RT "Double-stranded RNA interference shows that Engrailed controls the
RT synaptic specificity of identified sensory neurons.";
RL Curr. Biol. 10:1289-1292(2000).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AJ243885; CAB51043.1; -.
DR HSSP; P02836; 3HDD.
DR InterPro; IPR000747; Engrailed.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR000047; HTH_lanbrepresr.
DR Pfam; PF00046; homeobox; 1.
DR PRINTS; PR00026; ENGRAILED.
DR PRINTS; PR00024; HOMEBOX.
DR PRINTS; PR00031; HTHREPRESSR.
DR PRINTS; PR00010; Homeobox; 1.
DR ProDom; PD000010; Homeobox; 1.
DR SMART; SM00389; HOX; 1.
DR PROSITE; PS00033; ENGRAILED; 1.
DR PROSITE; PS00027; HOMEBOX; 1.
DR PROSITE; PS00071; HOMEBOX; 2; 1.
KW DNA-binding; Homeobox; Nuclear protein.
SQ SEQUENCE 211 AA; 23686 MW; 5886AB9B68685F2 CRC64;

Query Match 11.2%; Score 79.5; DB 5; Length 211;
Best Local Similarity 29.4%; Pred. No. 12;
Matches 32; Conservative 14; Mismatches 42; Indels 21; Gaps 5;

QY 43 ALAGMCGHVLPGTGSASAAVTPKGMKLP-----PRQSTKSPELRELGRK 93
Db 51 AIAGSPSSAV-PGASGSASGS-----GSSQLLPAWVYCTRYSDRPSGRSPSRMRKRK 105
QY 94 IREMNKT-----ISQESARVHRLPEGHPLLE-KAEYFRHLRLSKSQ 135
Db 106 DKPEKRPRTAFSGQLARLKHFTENRYLERRTELARELGINKAQ 154

RESULT 36
ID Q8VYQ4 PRELIMINARY; PRT; 348 AA.
AC Q8VYQ4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein (Atig24265/Atig24265).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Banh J., Bowser L.,
RA Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
RA Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RA Kim C.J., Chen H., Cheuk R., Meyers M.C., Shinn P., Banh J.,
RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis ORF clones.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY070135; AAL47485.1; -.
DR EMBL; AY103301; AAM65353.1; -.
DR InterPro; IPR000169; SHprot_acsite.

DR InterPro; IPR005829; Sug transporter.
DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.
DR PROSITE; PS00639; THIOLEPROTEASE_HIS; 1.
KW Hypothetical protein.
SQ SEQUENCE 348 AA; 37188 MW; 26F280470E4B8B2F CRC64;

Query Match 11.2%; Score 79.5; DB 10; Length 348;
Best Local Similarity 17.3%; Pred. No. 21;
Matches 22; Conservative 34; Mismatches 46; Indels 25; Gaps 4;

QY 8 TNFVAENRPTGETFDVVRREALRVKSERLAM--LRALAGMC-----GHRVLPFTG 57
Db 184 TSFIKDDVKAQVDAFENLASKVKVRIEGNQDITLFGVGLHAQCCQENRQIESNKALPST 243
QY 58 A--SAIAATVTPKGMKLPKPPRQSTKSPELRELRSK-----IREMNKTIS 102
Db 244 SLPALEAPMAPSSKTLUSLPASPDESQSPSTPNVAOKSRGLLOHTQSMGLKIDNESS 303
QY 103 QESARVN 109
Db 304 SHNTSSN 310

RESULT 37
ID Q9RKL6 PRELIMINARY; PRT; 357 AA.
AC Q9RKL6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein SCO4066.
GN SCO4066 OR SCD25.02.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A3(2) / M145;
RC MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Batenan A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Lark L., Murphy J., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2)." ;
RL Nature 417:141-147(2002).
DR EMBL; AL939118; CAB56346.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 357 AA; 39169 MW; 47249F754CAGF8A3 CRC64;

Query Match 11.2%; Score 79.5; DB 16; Length 357;
Best Local Similarity 33.3%; Pred. No. 22;
Matches 28; Conservative 10; Mismatches 29; Indels 17; Gaps 4;

QY 10 FVAENRP-----TFGETFDVVRREALRVKSERLAMLRALAGMCGHVRVLPFTGSAIA 62
Db 271 FVSDGPRVGLDQSTGGFTLPHARQALSRPDANH-----CGTC--RLRRAGLSAVG 321
QY 63 ATVTPKGMKLPKPP-RPQSTKSP 85
Db 322 AGPSTGASRKLRLPKLPSTPKGP 345

RESULT 38
ID Q9P4Z1 PRELIMINARY; PRT; 4065 AA.
AC Q9P4Z1;

01-OCT-2000 (Tremblrel. 15, Created)
01-DEC-2001 (Tremblrel. 19, Last sequence update)
01-MAR-2003 (Tremblrel. 23, Last annotation update)
Related to TOM1 protein.
B11B22.010.
GN Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.,
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AL356834; CAS92704.2; -
DR InterPro: IPR000569; HECT_domain.
DR Pfam: PF00632; HECT; 1.
DR SMART: SM00119; HECT; 1.
DR PROSITE: PS0237; HECT; 1.
SQ SEQUENCE 4065 AA; 452568 MW; F74683CEC36F9350 CRC64;
Query Match 11.2%; Score 79.5; DB 3; Length 4065;
Best Local Similarity 20.9%; Pred. No. 4.2e+02;
Matches 34; Conservative 26; Mismatches 50; Indels 53; Gaps 7;
Qy 16 PTFGETDVMREALLRVKSSER-----LAMLALAGCMGHRVLPFGTGAIAATVTP 67
Db 3570 PTFGKMDKLSACLSAIRQRDMNLNATILPLIESLMVCKNTL--SDASAVSNANSQ 3627
Qy 68 KGASMKLKPRPOS-----TKSPPELSRLR 92
Db 3628 K--EMLTSPPEPDRIAGLFTFTEEHRLNELVRHNPKLMGTFSLLVKNPKVLEFDN 3685
Qy 93 KIREMNTKISQESARVNHRLPEGHPL-LEKRAEYFRH--LRSL 132
Db 3686 KRYFNRSVHSKYQTRHSFP---PLQVRREHVHDSFRL 3725
RESULT 39
QY 01-MAY-1999 (Tremblrel. 10, Created)
ID Q9YP41, PRELIMINARY; PRT; 192 AA.
AC Q9YP41;
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Vif protein (Virion infectivity factor) (SOR protein).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA Fang G., Weiser B., Chappey C., Visosky A., Townsend L., Wang Q.,
RA Burger H.,
RT "Complete Plasma HIV-1 Sequence: Spl-Promoter Deletion Can Lead to
RT Non-Progressive Infection."
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: DETERMINES VIRUS INFECTION (BY SIMILARITY).
DR EMBL: U69589; A010913.1; -
DR InterPro: IPR000475; Viral_infect.
DR Pfam: PF00559; Vif; 1.
DR PRINTS: PR00349; VIRIONINFECT.
DR PRODOM: PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22434 MW; BB383D104E5A7A3E CRC64;
Query Match 11.2%; Score 79; DB 15; Length 192;
Best Local Similarity 29.0%; Pred. No. 11;
Matches 31; Conservative 10; Mismatches 28; Indels 38; Gaps 6;

QY 22 FDMREALLRVKSSERLAMLALAGCMGHRVLPG-----TGA-----SAIAATVTPKG 69
Db 112 FDCFSASAIR-----NAILGHRVSPSCYQAGHNKVGSLQVLAALAITPK- 157
QY 70 ASMKLKPRPOSQTSPELSRLRKIREMNTKISQESARVNHRLPEGH 116
Db 158 ---KIKPPLPSVTKLTEDR-----WNKPQTKGRGSHTM-NGH 192
RESULT 40
Q73093
ID Q73093, PRELIMINARY; PRT; 192 AA.
AC Q73093;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE Vif (viral infectivity factor) (Virion infectivity factor) (SOR protein).
GN VIF.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94303241; PubMed=8030283;
RA Wieland U., Hartmann J., Suhr H., Salzberger B., Eggers HJ.,
RA Kuehn J.E.;
RT "In vivo genetic variability of the HIV-1 vif gene."
RL Virology 203:43-51(1994).
CC -!- FUNCTION: DETERMINES VIRUS INFECTION (BY SIMILARITY).
DR EMBL: Z30605; CA83082.1; -
DR InterPro: IPR000475; Viral_infect.
DR Pfam: PF00559; Vif; 1.
DR PRINTS: PR00349; VIRIONINFECT.
DR PRODOM: PD000063; Viral_infect; 1.
KW AIDS.
SQ SEQUENCE 192 AA; 22317 MW; 2A48EFA3334900E CRC64;
Query Match 11.2%; Score 79; DB 15; Length 192;
Best Local Similarity 29.0%; Pred. No. 11;
Matches 31; Conservative 10; Mismatches 28; Indels 38; Gaps 6;
QY 22 FDMREALLRVKSSERLAMLALAGCMGHRVLPG-----TGA-----SAIAATVTPKG 69
Db 112 FDCFSASAIR-----NAILGHRVSPSCYQAGHNKVGSLQVLAALAITPK- 157
QY 70 ASMKLKPRPOSQTSPELSRLRKIREMNTKISQESARVNHRLPEGH 116
Db 158 ---KIKPPLPSVTKLTEDR-----WNKPQTKGRGSHTM-NGH 192
Search completed: November 14, 2003, 10:41:39
Job time : 71 secs

DM protein - protein search, using sw model

Run on: November 14, 2003, 10:42:41 ; Search time 41 Seconds
(without alignments)
545.865 Million cell updates/sec

Title: US-10-087-573-2
Perfect score: 141
Sequence: 1 MESTSTTNFVAENRPTFGE.....RAEYFRHLRLSKQGVNRLI 141

Scoring table: OJGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_19Jun03.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	126	89.4	285	23	ABP33715
3	7	5.0	16	24	ABP2389
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5	7	5.0	97	22	AAU46323
6	7	5.0	103	22	AAU46323
7	7	5.0	141	22	AAU46323
8	7	5.0	157	22	AAU46323
9	7	5.0	159	22	ABP33716
10	7	5.0	159	22	ABP33717
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12	7	5.0	159	22	ABP33719
13	7	5.0	159	22	ABP33720
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Propionibacterium
Drosophila melanog
Cryptosporidium sp
Novel human diago
Human novel protei
Human protein SEQ
Human protein SEQ
Human polypeptide
Melanocortin recep
Melanocortin recep
Human melanocortin
RPP5-like protein
Melanocortin-4 rec
Melanocortin-4 rec
Human melanocortin
Homo sapiens mutan
Homo sapiens mutan
Homo sapiens mutan
Human melanocortin
Sulfolobus solfata
Human melanocortin
Human MC4 protein.
A human melanocort
Human G protein co
Human G protein co
Rhesus monkey mela
Synthetic labeled
Melanocortin-4 rec
Amino acid sequenc
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Melanocortin recep
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Pseudomonas aerugi
Listeria monocytog
Chlamydomonas inte
Mycobacterium tube
Glycine max oil tr
Arabidopsis thalia
Aspergillus fumiga
E. coli cellular p
Arabidopsis thalia
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Aspergillus fumiga
Novel human diago
Drosophila melanog
Drosophila melanog
Subsequence which
Peptidomimetic of
Human C35 peptide
Human 34P3D7 HLA A
Human 34P3D7 HLA A
Troponin I peptide
Peptidomimetic of
Human HES 2 transc
Calmodulin inhibit
Human T lymphocyte
Polypeptide fragme
Human secreted pro
Human apo-lipoprot
Peptide #5053 enco
Peptide #5186 enco
Human AGE receptor
Human tropoelastin
Human tropoelastin
Human liver peptid
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Peptide #1611 enco
Protein #1542 enco
Human brain expres

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85	6	4.3	34	22	AAW27566	Peptide #1503 enco	158	6	4.3	76	20	AAV16642	WO9914235 Seg ID N
86	6	4.3	34	22	AAW02852	Peptide #1534 enco	159	6	4.3	76	22	AAU62764	Propionibacterium
87	6	4.3	34	23	ABG36921	Human peptide enco	160	6	4.3	77	21	AAU14470	Arabidopsis thalia
88	6	4.3	40	18	AAW20291	H. pylori cell env	161	6	4.3	77	22	ABG19038	Novel human diagno
89	6	4.3	40	21	AAW25024	Plant SDF encoded	162	6	4.3	77	23	ABBB8163	C bullatus mu-cono
90	6	4.3	41	15	AAW60064	Antimicrobial pept	163	6	4.3	78	22	AAO00583	Human polypeptide
91	6	4.3	41	16	AAW80734	Synthetic antimicr	164	6	4.3	78	23	ABP32744	Human ORF1717 prot
92	6	4.3	43	21	AAW25022	Plant SDF encoded	165	6	4.3	78	23	ABP01837	Human ORFX protein
93	6	4.3	44	21	AAW55117	Arabidopsis thalia	166	6	4.3	78	23	ABBB8165	C bullatus mu-cono
94	6	4.3	45	22	ABG54790	Human liver peptid	167	6	4.3	79	20	AAV19550	Amino acid sequenc
95	6	4.3	45	22	AAW73075	Human bone marrow	168	6	4.3	80	22	ABG13188	Novel human diagno
96	6	4.3	45	22	AAW85442	Human immune/haema	169	6	4.3	80	22	AAW91600	Human immune/haema
97	6	4.3	45	22	AAW33294	Peptide #7331 enco	170	6	4.3	81	21	AAW14469	Arabidopsis thalia
98	6	4.3	45	23	ABG42920	Human peptide enco	171	6	4.3	82	21	AAW08450	Arabidopsis thalia
99	6	4.3	51	22	ABG58273	Human liver peptid	172	6	4.3	82	23	ABP31546	Human ORF519 prote
100	6	4.3	51	22	ABBA42867	Peptide #10373 enco	173	6	4.3	83	21	AAV79172	P. carinii major s
101	6	4.3	51	22	ABBA61339	Protein #8138 enco	174	6	4.3	83	22	AAU65887	Propionibacterium
102	6	4.3	51	22	AAW63760	Human brain expres	175	6	4.3	84	22	AAU45110	Propionibacterium
103	6	4.3	51	22	AAW76574	Human bone marrow	176	6	4.3	84	22	AAU65766	Propionibacterium
104	6	4.3	51	22	AAW36681	Peptide #10718 enco	177	6	4.3	86	21	AAW53242	Human colon cancer
105	6	4.3	51	23	ABG45822	Human peptide enco	178	6	4.3	86	22	AAU56609	Propionibacterium
106	6	4.3	51	23	ABP09059	Human ORFX protein	179	6	4.3	87	22	ABW11339	Human beta-fibrino
107	6	4.3	52	22	ABG55673	Human liver peptid	180	6	4.3	88	22	AAW25265	Human protein sequ
108	6	4.3	52	22	ABBA40394	Peptide #7900 enco	181	6	4.3	89	23	ABG65221	Human albumin fusi
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116	6	4.3	55	20	AAW89089	Polypeptide fragme	189	6	4.3	97	22	AAU65570	Propionibacterium
117	6	4.3	55	21	ABG55116	Arabidopsis thalia	190	6	4.3	97	22	ABG91239	C glutamicum prote
118	6	4.3	55	22	ABG48446	Human liver peptid	191	6	4.3	101	23	ABR01707	Human breast speci
119	6	4.3	55	22	ABW28423	Peptide #1074 enco	192	6	4.3	104	21	AAW41199	Human ORFX ORF963
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122	6	4.3	55	22	ABW19059	Protein #1058 enco	195	6	4.3	106	21	AAW45788	Arabidopsis thalia
123	6	4.3	55	22	ABW02238	Human musculoskele	196	6	4.3	107	19	AAW75892	Peptide inhibitor
124	6	4.3	55	22	AAW54377	Human brain expres	197	6	4.3	107	19	AAW75895	Peptide inhibitor
125	6	4.3	55	22	AAW66778	Human bone marrow	198	6	4.3	107	21	AAW78860	Streptomycin subti
126	6	4.3	55	22	AAW14644	Peptide #1078 enco	199	6	4.3	107	23	ABP09234	Human ORFX protein
127	6	4.3	55	22	AAW27063	Peptide #1051 enco	200	6	4.3	110	21	AAW54411	Zea mays protein f
128	6	4.3	55	22	AAW02369	Medane and bHLH do	201	6	4.3	110	21	AAW00029	Human secreted pro
129	6	4.3	55	23	ABP52814	Human peptide enco	202	6	4.3	111	15	AAW60099	Antimicrobial prot
130	6	4.3	55	23	ABG36433	Novel human muscul	203	6	4.3	111	23	ABP09265	Human ORFX protein
131	6	4.3	55	24	ABU12532	Human immune/haema	204	6	4.3	113	22	AAU39573	Propionibacterium
132	6	4.3	56	22	AAW87268	Human immune/haema	205	6	4.3	114	22	AAU65156	Propionibacterium
133	6	4.3	58	21	AAW09191	Arabidopsis thalia	206	6	4.3	118	21	AAW00151	Human secreted pro
134	6	4.3	58	22	AAW58303	Propionibacterium	207	6	4.3	118	22	AAW01462	Human polypeptide
135	6	4.3	58	22	AAW89013	Human immune/haema	208	6	4.3	119	22	ABW68813	Drosophila melanog
136	6	4.3	58	22	ABP52813	Medane and bHLH do	209	6	4.3	120	21	AAW58812	Breast and ovarian
137	6	4.3	59	22	AAW99862	ERA binding domain	210	6	4.3	121	20	AAW49627	Corn hexose carrie
138	6	4.3	60	23	ABP00702	Human ORFX protein	211	6	4.3	121	21	AAW53892	Human colon cancer
139	6	4.3	61	18	AAW20768	H. pylori cell env	212	6	4.3	121	21	AAW18179	Arabidopsis thalia
140	6	4.3	62	22	ABW95797	Human testicular a	213	6	4.3	121	21	AAW45787	Arabidopsis thalia
141	6	4.3	62	22	AAW95092	Human reproductive	214	6	4.3	121	22	AAW01815	Human polypeptide
142	6	4.3	63	23	ABP38041	Staphylococcus epi	215	6	4.3	124	22	AAW81915	S. epidermidis ope
143	6	4.3	64	22	AAW52676	Propionibacterium	216	6	4.3	125	21	AAW18530	Zea mays protein f
144	6	4.3	64	22	ABG13937	Novel human diagno	217	6	4.3	126	21	AAW14595	Arabidopsis thalia
145	6	4.3	68	23	ABP08983	Human ORFX protein	218	6	4.3	126	20	AAW04508	Mycobacterium spec
146	6	4.3	68	24	ABW4698	Human DRHP riboso	219	6	4.3	128	23	ABU05760	M. tuberculosis an
147	6	4.3	69	21	AAW71961	Rat pituitary horm	220	6	4.3	128	23	ABU05760	Human protein sequ
148	6	4.3	69	22	AAW42690	Propionibacterium	221	6	4.3	129	23	ABP05151	Human ORFX protein
149	6	4.3	69	22	AAW80886	Human haematologic	222	6	4.3	131	14	AAW38222	Sequence of polype
150	6	4.3	69	22	AAW81352	Human haematologic	223	6	4.3	131	22	AAW95434	Human protein sequ
151	6	4.3	69	22	AAW81653	Human haematologic	224	6	4.3	135	21	AAW25407	Pinus radiata cell
152	6	4.3	69	22	AAW81895	Human haematologic	225	6	4.3	135	21	AAW19444	Arabidopsis thalia
153	6	4.3	70	21	AAW08451	Arabidopsis thalia	226	6	4.3	135	22	ABW69313	Drosophila melanog
154	6	4.3	70	21	ABW09457	L. helveticus exop	227	6	4.3	135	23	ABP34790	Human synthase-lik
155	6	4.3	71	23	ABW88631	Conus magus I-supe	228	6	4.3	135	23	AAW21290	Human Mrg (mas-rel

229 4.3 135 23 AAE21235 Human Mrg (mas-rel
230 4.3 136 13 AAR22387 Antigen tc-33c. E
231 4.3 140 22 AAU33273 Novel human secret
232 4.3 142 20 AAY08081 D. melanogaster SL
233 4.3 142 20 AAY08090 D. melanogaster SL
234 4.3 143 22 AAU19556 Human novel extrac
235 4.3 143 22 ABP47876 Human polypeptide
236 4.3 144 22 AAU63847 Propionibacterium
237 4.3 144 22 ABE54326 Lactococcus lactis
238 4.3 145 22 ABE66141 Drosophila melanog
239 4.3 149 21 AAY94985 Human secreted pro
240 4.3 150 21 AAG00150 Human secreted pro
241 4.3 151 23 ABUS1606 Helicobacter pylor
242 4.3 152 22 AAU18266 Human polypeptide
243 4.3 152 23 ABE84484 Consensus sodium/c
244 4.3 153 21 AAG14594 Arabidopsis thalia
245 4.3 153 23 ABE27677 Streptococcus poly
246 4.3 153 23 ABE29821 Streptococcus poly
247 4.3 158 19 AAY85930 S. pneumoniae deri
248 4.3 158 21 AAG57524 Arabidopsis thalia
249 4.3 158 24 AAU00803 S. pneumoniae type
250 4.3 160 20 AAY08082 D. melanogaster SL
251 4.3 161 20 AAY08091 D. melanogaster SL
252 4.3 161 21 AAG14593 Arabidopsis thalia
253 4.3 161 22 AAU31459 Novel human secret
254 4.3 162 21 AAG14427 Arabidopsis thalia
255 4.3 162 21 AAG38115 Arabidopsis thalia
256 4.3 162 22 ABE26172 Novel human diagno
257 4.3 163 23 ABP38264 Staphylococcus epi
258 4.3 164 22 AAG75966 Human colon cancer
259 4.3 165 21 AAG40093 Arabidopsis thalia
260 4.3 166 22 AAU37779 Streptococcus pneu
261 4.3 166 22 AAU38002 Streptococcus pneu
262 4.3 167 20 AAY48240 Human prostate can
263 4.3 168 22 AAU30445 Novel human secret
264 4.3 171 21 AAY69137 Amino acid sequenc
265 4.3 172 21 AAG57523 Arabidopsis thalia
266 4.3 173 20 AAU93961 Arabidopsis thalia
267 4.3 173 22 ABE82500 Human 53BP2:IP-1 P
268 4.3 176 22 AAU29219 Mouse prion-like m
269 4.3 176 22 AAU40040 Human PRO polypept
270 4.3 176 22 ABE82498 Human polypeptide
271 4.3 176 22 AAB70942 Human prion-like m
272 4.3 176 22 AAB70942 Human prion-relate
273 4.3 176 22 ABE87598 Human PRO3443. Ho
274 4.3 176 22 ABE49404 Human Dpl. Homo s
275 4.3 176 23 AAG95923 Human secreted/tra
276 4.3 176 24 ABU71307 Human PRO3443 prot
277 4.3 176 24 ABU71578 Human secreted pol
278 4.3 176 24 ABU72024 Novel human secret
279 4.3 176 24 ABU72181 Human PRO polypept
280 4.3 176 24 ABU65764 Human secreted/tra
281 4.3 176 24 ABU67601 Novel human secret
282 4.3 176 24 ABU67601 Novel human secret
283 4.3 176 24 ABUS58595 Human PRO polypept
284 4.3 176 24 ABUS56131 Human PRO polypept
285 4.3 176 24 ABUS71562 Human secreted/tra
286 4.3 176 24 ABU10705 Human secreted/tra
287 4.3 177 16 AAU00642 Infectious laryngo
288 4.3 177 17 AAU06794 ILTV unique short
289 4.3 177 22 AAU35519 Haemophilus influe
290 4.3 177 24 ABU00340 Human novel polype
291 4.3 178 22 ABE68838 Drosophila melanog
292 4.3 179 21 AAB42846 Human ORFX ORF2610
293 4.3 179 22 ABE50219 Human transcriptio
294 4.3 179 22 AAU39423 Human polypeptide
295 4.3 179 22 AAG33274 Human protein HP10
296 4.3 179 22 AAB82499 Mouse prion-like m
297 4.3 179 22 AAB70943 Murine prion-relat
298 4.3 179 22 AAB49405 Murine Dpl. Mus m
299 4.3 179 22 AAB49406 Rat Dpl. Rattus s
300 4.3 180 21 AAG14426 Arabidopsis thalia
301 4.3 180 21 AAG38114 Arabidopsis thalia

302 6 4.3 180 22 ABE69161 Drosophila melanog
303 6 4.3 181 22 AAU40197 Human polypeptide
304 6 4.3 181 22 AAB73688 Human oxidoreducta
305 6 4.3 182 15 AAR75690 Bacillus cereus ve
306 6 4.3 183 19 AAW98550 H. pylori GHPO 160
307 6 4.3 183 21 AAG40092 Arabidopsis thalia
308 6 4.3 183 21 AAG54281 Arabidopsis thalia
309 6 4.3 183 22 AAU33604 Pseudomonas aerugi
310 6 4.3 183 24 ABU18746 Pseudomonas aerugi
311 6 4.3 184 21 AAY95783 Erysipelatol protect
312 6 4.3 184 21 AAG54280 Arabidopsis thalia
313 6 4.3 184 22 AAG40775 Human polypeptide
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315 6 4.3 187 22 AAU40809 Propionibacterium
316 6 4.3 189 22 AAG91599 C glutamicum prote
317 6 4.3 190 22 ABE66385 Drosophila melanog
318 6 4.3 190 22 ABE66386 Drosophila melanog
319 6 4.3 190 22 AAU16299 Human novel secret
320 6 4.3 190 24 ABUS3568 Human novel polype
321 6 4.3 191 21 AAG51226 Arabidopsis thalia
322 6 4.3 192 23 ABP39484 Staphylococcus epi
323 6 4.3 193 22 ABE66021 Drosophila melanog
324 6 4.3 193 22 AAY37293 Protein involved i
325 6 4.3 194 20 AAY37293 Mouse pre-pro-neur
326 6 4.3 195 18 AAY16638 W0914235 Seq ID N
327 6 4.3 195 20 AAG35499 Arabidopsis thalia
328 6 4.3 198 21 AAG54279 Arabidopsis thalia
329 6 4.3 198 22 ABE69251 Drosophila melanog
330 6 4.3 200 20 AAY01305 Human tropoelastin
331 6 4.3 201 22 AAU16608 Human novel secret
332 6 4.3 201 22 ABE55677 Human novel polype
333 6 4.3 203 22 AAG90474 C glutamicum prote
334 6 4.3 204 23 ABE89705 Human polypeptide
335 6 4.3 206 20 AAY34855 Chlamydia pneumoni
336 6 4.3 206 21 AAG54279 Arabidopsis thalia
337 6 4.3 208 16 AAR77167 Arabidopsis thalia
338 6 4.3 209 22 AAU33956 Staphylococcus aur
339 6 4.3 209 22 AAU35789 Staphylococcus aur
340 6 4.3 209 22 AAU37387 Staphylococcus aur
341 6 4.3 210 21 AAG51225 Arabidopsis thalia
342 6 4.3 210 23 AAG97194 Polypeptide-riboso
343 6 4.3 211 22 AAU41983 Human polypeptide
344 6 4.3 212 21 AAB43169 Human ORFX ORF2933
345 6 4.3 212 22 AAU30621 Novel human secret
346 6 4.3 216 20 AAU01310 Human tropoelastin
347 6 4.3 216 22 AAU18225 Human DNA-B1
348 6 4.3 216 23 ABE92646 Human DNA-binding
349 6 4.3 216 23 ABP41748 Human ovarian anti
350 6 4.3 217 20 AAY35238 Amino acid sequenc
351 6 4.3 217 22 AAU62382 Propionibacterium
352 6 4.3 217 22 ABE10356 Human cDNA SEQ ID
353 6 4.3 217 23 ABP68943 Human polypeptide
354 6 4.3 221 22 AAU66542 Novel secreted pro
355 6 4.3 221 22 AAY97764 Propionibacterium
356 6 4.3 221 22 AAB81049 Human protein HP00
357 6 4.3 221 22 AAM39006 Human polypeptide
358 6 4.3 222 22 AAY34792 Chlamydia pneumoni
359 6 4.3 226 21 AAY2822 C. pneumoniae CPN1
360 6 4.3 227 23 ABE54979 Lactococcus lactis
361 6 4.3 228 22 ABE24267 Novel human diagno
362 6 4.3 228 24 ABE55597 DPP10 homologous p
363 6 4.3 229 21 AAG23447 Arabidopsis thalia
364 6 4.3 229 22 AAU59418 Propionibacterium
365 6 4.3 231 22 AAG91408 C glutamicum prote
366 6 4.3 231 22 AAB79561 Corynebacterium gl
367 6 4.3 232 20 AAY04809 Mycobacterium spec
368 6 4.3 233 21 AAG51224 Arabidopsis thalia
369 6 4.3 233 23 ABUS2175 Helicobacter pylor
370 6 4.3 235 21 AAB45275 Sequence #1 homolo
371 6 4.3 237 22 AAG83097 S. epidermidis ope
372 6 4.3 237 23 ABP39368 Staphylococcus epi
373 6 4.3 238 20 AAY00087 Enterococcus faeca
374 6 4.3 238 23 ABP43306 E faecalis EF040 a

375	238	23	ABP09432	Human ORFX protein	448	6	4.3	251	23	ABP44007	Human Blys binding
376	238	24	ABU13585	Enterococcus faeca	449	6	4.3	251	23	ABP44008	Human Blys binding
377	239	21	AAG4692	Zea mays protein f	450	6	4.3	251	23	ABP44009	Human Blys binding
378	239	22	AAG45311	Arabidopsis thalia	451	6	4.3	251	23	ABP44010	Human Blys binding
379	239	22	AAG18322	Human endocrine po	452	6	4.3	251	23	ABP44011	Human Blys binding
380	242	23	ABG65136	Human albumin fusi	453	6	4.3	251	23	ABP44012	Human Blys binding
381	242	23	ABP45819	Human Blys binding	454	6	4.3	251	23	ABP44013	Human Blys binding
382	242	23	ABP45833	Human Blys binding	455	6	4.3	251	23	ABP44014	Human Blys binding
383	242	23	ABP45803	Human secreted pro	456	6	4.3	251	23	ABP44015	Human Blys binding
384	243	23	ABP45504	Human Blys binding	457	6	4.3	251	23	ABP44016	Human Blys binding
385	243	23	ABP45522	Human Blys binding	458	6	4.3	251	23	ABP44017	Human Blys binding
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387	244	23	ABP45113	Human Blys binding	460	6	4.3	251	23	ABP44019	Human Blys binding
388	244	23	ABP45480	Human Blys binding	461	6	4.3	251	23	ABP44020	Human Blys binding
389	244	23	ABP45487	Human Blys binding	462	6	4.3	251	23	ABP44021	Human Blys binding
390	244	23	ABP45513	Human Blys binding	463	6	4.3	251	23	ABP44022	Human Blys binding
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393	244	23	ABP45571	Human Blys binding	466	6	4.3	251	23	ABP44025	Human Blys binding
394	244	23	ABP45834	Human Blys binding	467	6	4.3	251	23	ABP44026	Human Blys binding
395	245	23	ABP45505	Human Blys binding	468	6	4.3	251	23	ABP44027	Human Blys binding
396	245	23	ABP45512	Human Blys binding	469	6	4.3	251	23	ABP44028	Human Blys binding
397	245	23	ABP45510	Human Blys binding	470	6	4.3	251	23	ABP44029	Human Blys binding
398	245	23	ABP45517	Human Blys binding	471	6	4.3	251	23	ABP44030	Human Blys binding
399	245	23	ABP45521	Human Blys binding	472	6	4.3	251	23	ABP44031	Human Blys binding
400	245	23	ABP45536	Human Blys binding	473	6	4.3	251	23	ABP44032	Human Blys binding
401	245	23	ABP45539	Human Blys binding	474	6	4.3	251	23	ABP44033	Human Blys binding
402	245	23	ABP45828	Human Blys binding	475	6	4.3	251	23	ABP44034	Human Blys binding
403	245	23	ABP45849	Human Blys binding	476	6	4.3	251	23	ABP44035	Human Blys binding
404	246	23	ABP45823	Human Blys binding	477	6	4.3	251	23	ABP44036	Human Blys binding
405	247	22	AAU01661	Human secreted pro	478	6	4.3	251	23	ABP44044	Human Blys binding
406	247	22	ABP45481	Human Blys binding	479	6	4.3	251	23	ABP44050	Human Blys binding
407	247	23	ABP45700	Human Blys binding	480	6	4.3	251	23	ABP44053	Human Blys binding
408	248	21	AAV78931	Porcine melanocort	481	6	4.3	251	23	ABP44054	Human Blys binding
409	248	22	AAU08751	Porcine melanocort	482	6	4.3	251	23	ABP44056	Human Blys binding
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412	250	23	ABP44038	Human Blys binding	485	6	4.3	251	23	ABP44060	Human Blys binding
413	250	23	ABP44039	Human Blys binding	486	6	4.3	251	23	ABP44061	Human Blys binding
414	250	23	ABP44040	Human Blys binding	487	6	4.3	251	23	ABP44068	Human Blys binding
415	250	23	ABP44041	Human Blys binding	488	6	4.3	251	23	ABP44072	Human Blys binding
416	250	23	ABP44042	Human Blys binding	489	6	4.3	251	23	ABP44073	Human Blys binding
417	250	23	ABP44043	Human Blys binding	490	6	4.3	251	23	ABP44074	Human Blys binding
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421	250	23	ABP44047	Human Blys binding	494	6	4.3	251	23	ABP44078	Human Blys binding
422	250	23	ABP44048	Human Blys binding	495	6	4.3	251	23	ABP44079	Human Blys binding
423	250	23	ABP44049	Human Blys binding	496	6	4.3	251	23	ABP44080	Human Blys binding
424	250	23	ABP44051	Human Blys binding	497	6	4.3	251	23	ABP44081	Human Blys binding
425	250	23	ABP44052	Human Blys binding	498	6	4.3	251	23	ABP44082	Human Blys binding
426	250	23	ABP44055	Human Blys binding	499	6	4.3	251	23	ABP44083	Human Blys binding
427	250	23	ABP44058	Human Blys binding	500	6	4.3	251	23	ABP44084	Human Blys binding
428	250	23	ABP44062	Human Blys binding	501	6	4.3	251	23	ABP44085	Human Blys binding
429	250	23	ABP44064	Human Blys binding	502	6	4.3	251	23	ABP44086	Human Blys binding
430	250	23	ABP44065	Human Blys binding	503	6	4.3	251	23	ABP44087	Human Blys binding
431	250	23	ABP44066	Human Blys binding	504	6	4.3	251	23	ABP44088	Human Blys binding
432	250	23	ABP44067	Human Blys binding	505	6	4.3	251	23	ABP44090	Human Blys binding
433	250	23	ABP44069	Human Blys binding	506	6	4.3	251	23	ABP44091	Human Blys binding
434	250	23	ABP44070	Human Blys binding	507	6	4.3	251	23	ABP44092	Human Blys binding
435	250	23	ABP44079	Human Blys binding	508	6	4.3	251	23	ABP44093	Human Blys binding
436	250	23	ABP44080	Human Blys binding	509	6	4.3	251	23	ABP44095	Human Blys binding
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439	251	23	ABP43998	Human Blys binding	512	6	4.3	251	23	ABP44099	Human Blys binding
440	251	23	ABP43999	Human Blys binding	513	6	4.3	251	23	ABP44101	Human Blys binding
441	251	23	ABP44000	Human Blys binding	514	6	4.3	251	23	ABP44102	Human Blys binding
442	251	23	ABP44001	Human Blys binding	515	6	4.3	251	23	ABP44103	Human Blys binding
443	251	23	ABP44002	Human Blys binding	516	6	4.3	251	23	ABP44104	Human Blys binding
444	251	23	ABP44003	Human Blys binding	517	6	4.3	251	23	ABP44105	Human Blys binding
445	251	23	ABP44004	Human Blys binding	518	6	4.3	251	23	ABP44106	Human Blys binding
446	251	23	ABP44005	Human Blys binding	519	6	4.3	251	23	ABP44107	Human Blys binding
447	251	23	ABP44006	Human Blys binding	520	6	4.3	251	23	ABP44108	Human Blys binding

667	6	4.3	251	23	ABP44263	Human Blys binding	740	6	4.3	260	24	ABU71569	Human secreted pol
668	6	4.3	251	23	ABP44264	Human Blys binding	741	6	4.3	260	24	ABU72015	Novel human secret
669	6	4.3	251	23	ABP44265	Human Blys binding	742	6	4.3	260	24	ABU72172	Human PRO polypept
670	6	4.3	251	23	ABP44266	Human Blys binding	743	6	4.3	260	24	ABU65757	Human secreted/tra
671	6	4.3	251	23	ABP44267	Human Blys binding	744	6	4.3	260	24	ABU66090	Novel human secret
672	6	4.3	251	23	ABP44268	Human Blys binding	745	6	4.3	260	24	ABU67594	Human secreted/tra
673	6	4.3	251	23	ABP44269	Human Blys binding	746	6	4.3	260	24	ABU65452	Human PRO polypept
674	6	4.3	251	23	ABP44270	Human Blys binding	747	6	4.3	260	24	ABU58588	Human secreted/tra
675	6	4.3	251	23	ABP44271	Human Blys binding	748	6	4.3	260	24	ABU56124	Human secreted/tra
676	6	4.3	251	23	ABP44272	Human Blys binding	749	6	4.3	260	24	ABU56722	Lung cancer-associ
677	6	4.3	251	23	ABP44273	Human Blys binding	750	6	4.3	260	24	ABU57119	Human PRO polypept
678	6	4.3	251	23	ABP44274	Human Blys binding	751	6	4.3	260	24	ABR00094	Human gene 84 enco
679	6	4.3	251	23	ABP44275	Human Blys binding	752	6	4.3	260	24	ABU10698	Human secreted/tra
680	6	4.3	251	23	ABP44276	Human Blys binding	753	6	4.3	261	22	ABG15226	Novel human diago
681	6	4.3	251	23	ABP44277	Human Blys binding	754	6	4.3	261	22	ABP40090	Staphylococcus epi
682	6	4.3	251	23	ABP44278	Human Blys binding	755	6	4.3	262	21	AAV71962	Consensus sequenc
683	6	4.3	251	23	ABP44279	Human Blys binding	756	6	4.3	262	22	ABU10216	Human CDNA SEQ ID
684	6	4.3	251	23	ABP44280	Human Blys binding	757	6	4.3	262	22	AAU23023	Novel human enzym
685	6	4.3	251	23	ABP44281	Human Blys binding	758	6	4.3	262	22	AAU18448	Human endocrine po
686	6	4.3	251	23	ABP44282	Human Blys binding	759	6	4.3	262	22	ABP66803	Human polypeptide
687	6	4.3	251	23	ABP44283	Human Blys binding	760	6	4.3	262	20	AAV19757	SEQ ID NO 475 from
688	6	4.3	251	23	ABP44284	Human Blys binding	761	6	4.3	264	21	AAV66637	Membrane-bound pro
689	6	4.3	251	23	ABP44285	Human Blys binding	762	6	4.3	264	21	AAV57942	Human transmembran
690	6	4.3	251	23	ABP44286	Human Blys binding	763	6	4.3	264	21	AAU29029	Human PRO polypept
691	6	4.3	251	23	ABP44287	Human Blys binding	764	6	4.3	264	22	AAU78410	Human protein SEQ
692	6	4.3	251	23	ABP44288	Human Blys binding	765	6	4.3	264	22	AAU65160	Human PRO194 (UNQ
693	6	4.3	251	23	ABP44289	Human Blys binding	766	6	4.3	264	23	ABU79335	Human ovary specif
694	6	4.3	251	23	ABP44290	Human Blys binding	767	6	4.3	264	23	ABU89985	Human polypeptide
695	6	4.3	251	23	ABP44291	Human Blys binding	768	6	4.3	264	24	ABU71117	Human PRO194 prote
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697	6	4.3	251	23	ABP44293	Human Blys binding	770	6	4.3	264	24	ABU65907	Novel human secret
698	6	4.3	251	23	ABP44294	Human Blys binding	771	6	4.3	264	24	ABU67411	Human secreted/tra
699	6	4.3	251	23	ABP44295	Human Blys binding	772	6	4.3	264	24	ABU65269	Human PRO polypept
700	6	4.3	251	23	ABP44296	Human Blys binding	773	6	4.3	264	24	ABU59053	Novel human secret
701	6	4.3	251	23	ABP44297	Human Blys binding	774	6	4.3	264	24	ABU59200	Human secreted/tra
702	6	4.3	251	23	ABP44298	Human Blys binding	775	6	4.3	264	24	ABU59349	Novel human secret
703	6	4.3	251	23	ABP44299	Human Blys binding	776	6	4.3	264	24	ABU60484	Human secreted/tra
704	6	4.3	251	23	ABP44300	Human Blys binding	777	6	4.3	264	24	ABU57975	Human PRO polypept
705	6	4.3	251	23	ABP44301	Human Blys binding	778	6	4.3	264	24	ABU58405	Human PRO polypept
706	6	4.3	251	23	ABP44302	Human Blys binding	779	6	4.3	264	24	ABU58906	Human secreted/tr
707	6	4.3	251	23	ABP44303	Human Blys binding	780	6	4.3	264	24	ABU55941	Human secreted/tra
708	6	4.3	251	23	ABP44304	Human Blys binding	781	6	4.3	264	24	ABU56936	Human PRO194 polyp
709	6	4.3	251	23	ABP44305	Human Blys binding	782	6	4.3	264	24	ABU13866	Human secreted/tra
710	6	4.3	251	23	ABP44306	Human Blys binding	783	6	4.3	264	24	ABU10515	Human PRO polypept
711	6	4.3	251	23	ABP44307	Human Blys binding	784	6	4.3	266	21	AAU10821	Human PRO polypept
712	6	4.3	251	23	ABP44308	Human Blys binding	785	6	4.3	266	21	AAU41735	Human ORFX ORF1499
713	6	4.3	251	23	ABP44309	Human Blys binding	786	6	4.3	267	20	ABG70509	Enterococcus faeca
714	6	4.3	251	23	ABP44310	Human Blys binding	787	6	4.3	267	23	ABG70509	Human ribosome S11
715	6	4.3	251	23	ABP44311	Human Blys binding	788	6	4.3	267	23	ABP43305	E faecalis EF040 p
716	6	4.3	251	23	ABP44312	Human Blys binding	789	6	4.3	267	23	ABP43305	Human secreted pro
717	6	4.3	251	23	ABP44313	Human Blys binding	790	6	4.3	267	24	ABU13584	Human secreted pro
718	6	4.3	251	23	ABP44314	Human Blys binding	791	6	4.3	272	21	AAU77124	Human neurotransmi
719	6	4.3	251	23	ABP44315	Human Blys binding	792	6	4.3	272	23	ABU51878	Helicobacter pylor
720	6	4.3	251	23	ABP44316	Human Blys binding	793	6	4.3	274	22	AAU05258	Dog stem cell fact
721	6	4.3	251	23	ABP44317	Human Blys binding	794	6	4.3	274	22	AAU05258	Dog SCF protein SE
722	6	4.3	251	23	ABP44318	Human Blys binding	795	6	4.3	274	22	AAU02485	Dog SCF (stem cell
723	6	4.3	251	23	ABP44319	Human Blys binding	796	6	4.3	274	22	AAU02771	Dog SCF (stem cell
724	6	4.3	251	23	ABP44320	Human Blys binding	797	6	4.3	274	22	AAU02771	Dog SCF (stem cell
725	6	4.3	251	23	ABP44321	Human Blys binding	798	6	4.3	274	22	AAU02771	Dog stem cell fact
726	6	4.3	251	23	ABP44322	Human Blys binding	799	6	4.3	275	23	ABP25835	Streptococcus poly
727	6	4.3	251	23	ABP44323	Human Blys binding	800	6	4.3	275	23	ABP25835	Listeria monocytog
728	6	4.3	251	23	ABP44324	Human Blys binding	801	6	4.3	276	21	ABU58995	Arabidopsis circad
729	6	4.3	251	23	ABP44325	Human Blys binding	802	6	4.3	276	22	ABU11763	Human REM2 homolog
730	6	4.3	251	23	ABP44326	Human Blys binding	803	6	4.3	276	22	AAU79740	Human protein SEQ
731	6	4.3	251	23	ABP44327	Human Blys binding	804	6	4.3	277	22	ABU11893	Human novel protei
732	6	4.3	251	23	ABP44328	Human Blys binding	805	6	4.3	277	22	ABU11893	Human protein SEQ
733	6	4.3	251	23	ABP44329	Human Blys binding	806	6	4.3	280	21	AAU19933	Arabidopsis thalia
734	6	4.3	251	23	ABP44330	Human Blys binding	807	6	4.3	280	21	AAU19933	Arabidopsis thalia
735	6	4.3	251	23	ABP44331	Human Blys binding	808	6	4.3	281	21	AAU39370	Gene 18 human secr
736	6	4.3	251	23	ABP44332	Human Blys binding	809	6	4.3	281	21	AAU39371	Human secreted pro
737	6	4.3	251	23	ABP44333	Human Blys binding	810	6	4.3	281	21	AAU19932	Arabidopsis thalia
738	6	4.3	251	23	ABP44334	Human Blys binding	811	6	4.3	281	21	AAU32365	Arabidopsis thalia
739	6	4.3	251	23	ABP44335	Human Blys binding	812	6	4.3	281	22	AAU39133	Putative deoxyribo

813	6	4.3	282	21	AAG19931	Arabidopsis thalia	886	6	4.3	342	20	AAW99021	Chlamydia trachom
814	6	4.3	282	21	AAG32364	Arabidopsis thalia	887	6	4.3	343	14	AAW41670	Porcine sialytra
815	6	4.3	282	22	AUJ36009	Helicobacter pylor	888	6	4.3	343	16	AAW65240	Porcine ST30 sialy
816	6	4.3	282	21	AAE02488	Arabidopsis thalia	889	6	4.3	344	22	AAW90406	C glutamicum prote
817	6	4.3	284	21	AAE43822	Human cancer assoc	890	6	4.3	344	22	AAW79096	Corynebacterium gl
818	6	4.3	285	22	ABG13938	Novel human diagn	891	6	4.3	344	24	ABW78043	N. gonorrhoeae ami
819	6	4.3	285	23	ABG91576	Purine/pyrimidine	892	6	4.3	345	23	AAW15493	Beta vulgaris dihy
820	6	4.3	288	20	AAW29081	T. gondii immunoge	893	6	4.3	346	22	AAW15493	Potato dihydro-oro
821	6	4.3	288	20	AAW29082	T. gondii immunoge	894	6	4.3	346	22	AAW70773	Potato dihydro-oro
822	6	4.3	288	22	AAU25552	T. gondii immunoge	895	6	4.3	348	21	AAW23446	Arabidopsis thalia
823	6	4.3	288	22	AAU25553	T. gondii immunoge	896	6	4.3	348	21	AAW44691	Zea mays protein f
824	6	4.3	288	22	ABU54054	Lactococcus lactis	897	6	4.3	348	22	AAW68968	Drosophila melanog
825	6	4.3	289	22	AAW66463	Protein encoded by	898	6	4.3	349	8	AAW70463	Sequence of gpi en
826	6	4.3	290	20	AAW42389	Amino acid sequenc	899	6	4.3	353	21	AAW55869	Arabidopsis thalia
827	6	4.3	290	22	AAU39081	Human secreted pro	900	6	4.3	353	21	AAW61589	Arabidopsis thalia
828	6	4.3	290	23	AAO18610	Synechocystis HhoA	901	6	4.3	353	22	ABW63007	Drosophila melanog
829	6	4.3	290	23	ABW55790	Human polypeptide	902	6	4.3	357	20	AAW35069	Chlamydia pneumoni
830	6	4.3	292	24	ABU56537	Lung cancer-associ	903	6	4.3	359	20	AAW44336	Human cell surface
831	6	4.3	293	22	ABW69343	Drosophila melanog	904	6	4.3	359	20	AAW41690	Human PRO329 prote
832	6	4.3	293	22	ABG26384	Novel human diagn	905	6	4.3	359	21	AAW44246	Human secreted pro
833	6	4.3	293	23	ABW59039	Ribosyltransferase	906	6	4.3	359	21	AAW34444	Human secreted pro
834	6	4.3	294	17	AAW88003	Delta-endotoxin MK	907	6	4.3	359	21	AAW55868	Human secreted/tr
835	6	4.3	294	22	ABW69400	Drosophila melanog	908	6	4.3	359	21	AAW61588	Arabidopsis thalia
836	6	4.3	296	22	AAW79448	Human protein SEQ	909	6	4.3	359	22	AAW29044	Human PRO polypept
837	6	4.3	296	23	ABP43778	FLJ14840 fis clone	910	6	4.3	359	22	AAW633451	Human gene 25 enco
838	6	4.3	296	23	ABG91476	Purine/pyrimidine	911	6	4.3	359	23	AAW63386	Human albumin fusi
839	6	4.3	297	23	ABW90648	Chlamydia pneumoni	912	6	4.3	359	24	ABW47894	Human secreted pro
840	6	4.3	300	24	ABP78818	N. gonorrhoeae ami	913	6	4.3	359	24	ABU71132	Human PRO329 prote
841	6	4.3	305	21	AAW55870	Arabidopsis thalia	914	6	4.3	359	24	AAW55589	Human secreted/tr
842	6	4.3	305	21	AAW61590	Arabidopsis thalia	915	6	4.3	359	24	ABU65922	Novel human secret
843	6	4.3	306	22	ABW62221	Drosophila melanog	916	6	4.3	359	24	ABU67426	Human secreted/tr
844	6	4.3	307	22	AAW38989	Human polypeptide	917	6	4.3	359	24	ABU61076	Human PRO329 polyp
845	6	4.3	307	22	AAW93665	Human protein sequ	918	6	4.3	359	24	ABU65284	Human PRO polypept
846	6	4.3	307	22	AAW36211	Human immune syste	919	6	4.3	359	24	ABU58420	Human PRO polypept
847	6	4.3	307	23	ABP65088	Hypoxia-repressed	920	6	4.3	359	24	ABU58420	Human secreted/tr
848	6	4.3	307	23	ABW90186	Human polypeptide	921	6	4.3	359	24	ABU55956	Human PRO polypept
849	6	4.3	309	22	ABW67282	Drosophila melanog	922	6	4.3	359	24	ABU55956	Human secreted/tr
850	6	4.3	314	22	AAW80387	Secreted protein e	923	6	4.3	359	24	ABU00153	Human gene 143 enc
851	6	4.3	314	23	ABG65288	Aspergillus fumiga	924	6	4.3	359	24	ABU10530	Human secreted/tr
852	6	4.3	315	24	ABJ25914	Aspergillus fumiga	925	6	4.3	360	24	ABW78133	N. gonorrhoeae ami
853	6	4.3	315	24	ABJ26514	C. acetobutylicum	926	6	4.3	361	21	AAW41628	Human ORFX ORF1392
854	6	4.3	318	20	AAW95502	Salmonella typhi c	927	6	4.3	361	21	AAW41628	Arabidopsis thalia
855	6	4.3	318	22	AAU38156	Human A33 antigen	928	6	4.3	361	22	AAW82410	S. epidermidis ope
856	6	4.3	319	18	AAW14146	Human A33 antigen	929	6	4.3	365	23	ABW69786	Human polypeptide
857	6	4.3	319	20	AAW23323	Amino acid sequenc	930	6	4.3	368	18	AAW21561	Novel human diagn
858	6	4.3	319	22	AAW65883	Human A33 protein	931	6	4.3	370	22	AAW51676	T. neopolitana Xyn
859	6	4.3	321	22	AAU34490	E. coli cellular p	932	6	4.3	372	23	AAW79570	Propionibacterium
860	6	4.3	322	22	AAW983356	Escherichia coli p	933	6	4.3	373	15	AAW48703	G-protein coupled
861	6	4.3	326	17	AAW06325	Dihydrodipicolinic	934	6	4.3	373	17	AAW02675	G-protein coupled
862	6	4.3	327	19	AAW60220	Bacillus thuringie	935	6	4.3	374	21	AAW05905	Mouse brain staliid
863	6	4.3	327	19	AAW60223	Bacillus thuringie	936	6	4.3	374	21	AAW12962	G-protein coupled
864	6	4.3	327	19	AAW90286	Human peptidase, H	937	6	4.3	375	24	ABW73019	Arabidopsis thalia
865	6	4.3	327	22	AAE03647	Human extracellular	938	6	4.3	375	24	ABW70707	Amino acid sequenc
866	6	4.3	328	22	AAU35731	Helicobacter pylor	939	6	4.3	377	21	AAW20649	Paenibacillus hexe
867	6	4.3	331	20	AAV37504	Protein involved i	940	6	4.3	377	21	AAW45918	Arabidopsis thalia
868	6	4.3	331	22	AAU46431	Propionibacterium	941	6	4.3	378	22	ABW03493	Novel human diagn
869	6	4.3	331	22	AAU55394	Propionibacterium	942	6	4.3	378	22	AAW93936	Human polypeptide
870	6	4.3	331	22	ABG18006	Novel human diagn	943	6	4.3	378	22	AAW93936	Human polypeptide
871	6	4.3	332	21	AAW55461	Arabidopsis thalia	944	6	4.3	378	23	ABW92716	Herbicidally activ
872	6	4.3	332	22	AAW90554	C glutamicum prote	945	6	4.3	378	24	AAO19572	M sterilia protein
873	6	4.3	332	23	AAU79516	Corynebacterium gl	946	6	4.3	380	17	AAW06326	DHPS:chloroplast t
874	6	4.3	332	23	AAU76427	Feline melanocorti	947	6	4.3	380	21	AAW24234	Arabidopsis thalia
875	6	4.3	332	23	AAU76428	Canine melanocorti	948	6	4.3	380	21	AAW24234	Arabidopsis thalia
876	6	4.3	333	21	AAW30942	Arabidopsis thalia	949	6	4.3	380	21	AAW39915	Arabidopsis thalia
877	6	4.3	335	23	ABP30343	Streptococcus poly	950	6	4.3	380	23	ABW93230	Herbicidally activ
878	6	4.3	336	23	ABW2881	Human polypeptide	951	6	4.3	381	21	AAW20525	Arabidopsis thalia
879	6	4.3	337	22	ABG18204	Novel human diagn	952	6	4.3	381	22	AAU33416	Enterococcus faeca
880	6	4.3	338	23	ABW57357	Mouse ischaemic co	953	6	4.3	382	23	ABW75676	Human D1AR-V2R pol
881	6	4.3	339	20	AAV35649	Chlamydia pneumoni	954	6	4.3	383	15	AAW56166	Neuroendocrine tum
882	6	4.3	340	23	ABP28097	Streptococcus poly	955	6	4.3	383	24	ABU12063	Human NOV11a CG916
883	6	4.3	340	23	ABP29857	S. pneumoniae type	956	6	4.3	384	22	ABU12064	Human NOV11b CG916
884	6	4.3	340	24	ABU02808	Arabidopsis thalia	957	6	4.3	384	22	ABW99128	Murine G protein-cou
885	6	4.3	341	21	AAW55460	Arabidopsis thalia	958	6	4.3	386	22	ABW63549	Drosophila melanog

959 Murine adrenergic
960 Fusarium oxysporum
961 Arabidopsis thalia
962 Arabidopsis thalia
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999 Arabidopsis thalia
1000 Arabidopsis thalia

ALIGNMENTS

RESULT 1
ABP53714
ID ABP53714 standard; Protein; 141 AA.
XX
AC ABP53714;
XX
DT 23-DEC-2002 (first entry)
XX
DE Babesia canis BcVir15 15kD protein SEQ ID NO:2.
XX
KW Babesia canis; BcVir15; 15kD protein; BcVir32; 32kD protein; infection;
KW antiparasitic; immunostimulant; vaccine.
XX
OS Babesia canis.
XX
PN EPI238983-A1.
XX
PD 11-SEP-2002.
XX
PF 04-MAR-2002; 2002EP-0075830.
XX
PR 06-MAR-2001; 2001EP-0200816.
XX
PA (ALKU) AKZO NOBEL NV.
XX
PI Schettlers TPM, Carcy BPD, Drakulovski PR, Gorenflot AF;

XX WPI: 2002-724917/79.
DR N-FSDB; ABQ82649.
XX
PT Novel Babesia canis associated protein and nucleic acid encoding the
PT protein, useful in a vaccine and in the manufacture of vaccines for
PT combating Babesia canis infections
XX
XX Claim 1; Fig 2; 4lpp; English.
XX
CC The present invention describes a Babesia canis associated protein (I),
CC comprising a BcVir15 protein of 15 kD molecular weight (MW) and having
CC a sequence of at least 80% homology to a sequence (ABP53714) of 141
CC amino acids, or a BcVir32 protein of 32 kD MW and having a sequence of
CC at least 80% homology to a sequence (ABP53715) of 285 amino acids, or
CC their immunogenic fragments. (I) have antiparasitic and immunostimulant
CC activities, and can be used in vaccines. (I) can also be used for the
CC preparation of a vaccine for combating B. canis infections. (I) is also
CC useful in a diagnostic test for the detection of antibodies against
CC B. canis associated antigenic material. The present sequence represents
CC BcVir15 from the present invention.
XX
SQ Sequence 141 AA;
Query Match 100.0%; Score 141; DB 23; Length 141;
Best Local Similarity 100.0%; Pred. No. 4.2e-137; Indels 0; Gaps 0;
Matches 141; Conservative 0; Mismatches 0;
QY 1 MESTSTTTNFVAENRPTFGTDFVMEALLRVKSSERLALMRLAGMCGHRVLPGTGASA 60
DB 1 MESTSTTTNFVAENRPTFGTDFVMEALLRVKSSERLALMRLAGMCGHRVLPGTGASA 60
QY 61 IAAVTTPKASMKLKPFRPOSTKSPLELSRKIRENMKTIQESARVNHRLPEGHILLE 120
DB 61 IAAVTTPKASMKLKPFRPOSTKSPLELSRKIRENMKTIQESARVNHRLPEGHILLE 120
QY 121 KRAEYFRHLRSLKSGQVNRLLI 141
DB 121 KRAEYFRHLRSLKSGQVNRLLI 141
RESULT 2
ABP53715
ID ABP53715 standard; Protein; 285 AA.
XX
AC ABP53715;
XX
DT 23-DEC-2002 (first entry)
XX
DE Babesia canis BcVir32 32kD protein SEQ ID NO:4.
XX
KW Babesia canis; BcVir15; 15kD protein; BcVir32; 32kD protein; infection;
KW antiparasitic; immunostimulant; vaccine.
XX
OS Babesia canis.
XX
PN EPI238983-A1.
XX
PD 11-SEP-2002.
XX
PF 04-MAR-2002; 2002EP-0075830.
XX
PR 06-MAR-2001; 2001EP-0200816.
XX
PA (ALKU) AKZO NOBEL NV.
XX
PI Schettlers TPM, Carcy BPD, Drakulovski PR, Gorenflot AF;
XX
XX WPI: 2002-724917/79.
DR N-FSDB; ABQ82650.
XX
PT Novel Babesia canis associated protein and nucleic acid encoding the
PT protein, useful in a vaccine and in the manufacture of vaccines for

PT combating Babesia canis infections -
PS Claim 2; Fig 3; 41pp; English.
XX
CC The present invention describes a Babesia canis associated protein (I),
CC comprising a BcVir15 protein of 15 kD molecular weight (MW) and having
CC a sequence of at least 80% homology to a sequence (ABP53714) of 141
CC amino acids, or a BcVir12 protein of 32 kD MW and having a sequence of
CC at least 80% homology to a sequence (ABP53715) of 285 amino acids, or
CC their immunogenic fragments. (I) have antiparasitic and immunostimulant
CC activities, and can be used in vaccines. (I) can also be used for the
CC preparation of a vaccine for combating B. canis infections. (I) is also
CC useful in a diagnostic test for the detection of antibodies against
CC B. canis associated antigenic material. The present sequence represents
CC BcVir32 from the present invention.
XX
SQ Sequence 285 AA;
Query Match 89.4%; Score 126; DB 23; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.4e-121; Indels 0; Gaps 0;
Matches 126; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MESTTTTNFVAENRPTFGETPDVNRALLRVKSSERLAMLALAGMCHRVLPQTGASA 60
DB 1 MESTTTTNFVAENRPTFGETPDVNRALLRVKSSERLAMLALAGMCHRVLPQTGASA 60
QY 61 IAATVTPKGASKMLAPPRQSTKSPRLRLSKIREMKNKTSQESARVNHRLPEGHPLLE 120
DB 61 IAATVTPKGASKMLAPPRQSTKSPRLRLSKIREMKNKTSQESARVNHRLPEGHPLLE 120
QY 121 KRAEYF 126
DB 121 KRAEYF 126

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating
PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,
PT cancer or autoimmune diseases -
XX
PS Claim 1; Fig 2; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising:
CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular
CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity
CC or avidity for a particular GPCR. (I) can be used as GPCR modulators and
CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting
CC an antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related diseases, immunological-related diseases, cell
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention.
XX
SQ Sequence 16 AA;
Query Match 5.0%; Score 7; DB 24; Length 16;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 52 VLPQTGA 58
DB 5 VLPQTGA 11
RESULT 4
AAU46323
ID AAU46323 standard; Protein; 88 AA.
XX
AC AAU46323;
XX
DT 27-FEB-2002 (first entry)
XX
DE Propionibacterium acnes immunogenic protein #7219.
XX
KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant.
XX
OS Propionibacterium acnes.
XX
PN WO200181581-A2.
XX
PD 01-NOV-2001.
XX
PF 20-APR-2001; 2001WO-US12865.
XX
PR 21-APR-2000; 2000US-199047P.
PR 02-JUN-2000; 2000US-208841P.
PR 07-JUL-2000; 2000US-216747P.
XX
PA (CORI-) CORIXA CORP.
XX

PI Skeiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
XX WPI; 2001-616774/71.
DR N-PSDB; AA859531.
XX
PT Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
PS Example 1; SEQ ID No 7518; 1069pp; English.
XX
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 88 AA;
SQ
Query Match 5.0%; Score 7; DB 22; Length 88;
Best Local Similarity 100.0%; Pred. No. 36;
Matches. 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 111 RLPEGHP 117
Db 66 RLPEGHP 72
RESULT 5
AAM85765
ID AAM85765 standard; Protein; 97 AA.
XX
AC AAM85765;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen SEQ ID NO:13358.
XX
DE Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX
KW cytostatic; gene therapy; vaccine; metastasis.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PN 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR
07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214896.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 30-AUG-2000; 2000US-0227009.
PR 01-SEP-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0232081.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 13-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.

20-OCT-2000;	2000US-0241785.
20-OCT-2000;	2000US-0241786.
20-OCT-2000;	2000US-0241787.
20-OCT-2000;	2000US-0241808.
20-OCT-2000;	2000US-0241809.
20-OCT-2000;	2000US-0241826.
01-NOV-2000;	2000US-024617.
08-NOV-2000;	2000US-0246474.
08-NOV-2000;	2000US-0246475.
08-NOV-2000;	2000US-0246476.
08-NOV-2000;	2000US-0246477.
08-NOV-2000;	2000US-0246478.
08-NOV-2000;	2000US-0246523.
08-NOV-2000;	2000US-0246524.
08-NOV-2000;	2000US-0246525.
08-NOV-2000;	2000US-0246526.
08-NOV-2000;	2000US-0246527.
08-NOV-2000;	2000US-0246528.
08-NOV-2000;	2000US-0246532.
08-NOV-2000;	2000US-0246609.
08-NOV-2000;	2000US-0246610.
08-NOV-2000;	2000US-0246611.
08-NOV-2000;	2000US-0246613.
17-NOV-2000;	2000US-0249207.
17-NOV-2000;	2000US-0249208.
17-NOV-2000;	2000US-0249209.
17-NOV-2000;	2000US-0249210.
17-NOV-2000;	2000US-0249211.
17-NOV-2000;	2000US-0249212.
17-NOV-2000;	2000US-0249213.
17-NOV-2000;	2000US-0249214.
17-NOV-2000;	2000US-0249215.
17-NOV-2000;	2000US-0249216.
17-NOV-2000;	2000US-0249217.
17-NOV-2000;	2000US-0249218.
17-NOV-2000;	2000US-0249244.
17-NOV-2000;	2000US-0249245.
17-NOV-2000;	2000US-0249264.
17-NOV-2000;	2000US-0249265.
17-NOV-2000;	2000US-0249297.
17-NOV-2000;	2000US-0249299.
17-NOV-2000;	2000US-0249300.
01-DEC-2000;	2000US-0250160.
01-DEC-2000;	2000US-0250391.
05-DEC-2000;	2000US-0251030.
05-DEC-2000;	2000US-0251988.
05-DEC-2000;	2000US-0256719.
06-DEC-2000;	2000US-0251479.
08-DEC-2000;	2000US-0251856.
08-DEC-2000;	2000US-0251868.
08-DEC-2000;	2000US-0251869.
08-DEC-2000;	2000US-0251889.
08-DEC-2000;	2000US-0251990.
11-DEC-2000;	2000US-0254097.
05-JAN-2001;	2001US-0259678.
(HUMA-) HUMAN GENOME SCI INC.	
Rosen CA, Baraesh SC, Ruben SM;	
WPI; 2001-483426/52.	
N-PSDB; AAK58546.	
Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -	
Claim 11; SEQ ID NO 13358; 3071bp + Sequence Listing; English.	
AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAK52170 to AAK51921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and	

CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
XX Sequence 97 AA;

Sequence 97 AA;

Query Match 5.0%; Score 7; DB 22; Length 97;

Query Match	5.00%	Score 7	Length 20
Best Local Similarity	100.0%	Pred. No. 40	
Matches	7	Conservative	0
Mismatches	0	Indels	0
Gaps	0		

Qy 51 RVLPGTG 57

[illegible]

RESULT 6

ABP09535
ID ABP09535 standard; Protein; 103 AA.

AX
AC ABP09535:

DT 24-JUN-2002 (first entry)
XX ABF09333;
RC

DE Human ORFX protein sequence SEQ ID NO:19052. XX

Human; open reading frame; ORF; gene therapy; cancer; cirrhosis; hyperplastic disorder; psoriasis; benign tumour; haemorrhage; degenerative disease; osteoarthritis; neurodegenerative disorder; cystic fibrosis; atherosclerosis; cholesterol ester storage; demyelination; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis

XX Homo sapiens.

AA
PN
WO200192523-A2XX
PD
06-DEC-2001XX
PF 29-MAY-2001; 2001WO-US10836.

XX
PR 30-MAY-2000: 2000US-206132P.

PR 29-AUG-2000; 2000US-228/16P.
XX

XX
PA (CURA-) CURAGEN CORP.

AA Shimkets RA. Leach MD:

XX
DR WPI: 2002-106308/14.

DR N-PSDB; ABN25287.
XX

PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and autoimmune disorders.
PT novel human polypeptides and polynucleotides useful for diagnosing,

XX
PS Disclosure: SEC ID 10052: 103700. English

xx
CC The present invention describes substantially purified human proteins
CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
CC in the specification). ABN15762 to ABN27252 encode the human ORFX
CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
CC treating or preventing a pathology associated with an ORFX-associated

CC disorder in humans, and in the manufacture of a medicament for treating a
CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
CC sequences can be used in gene therapy. ORFX sequences can be used in the
CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
CC osteoarthritis, neurodegenerative disorders, disorders related to organ
CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
CC storage disease, various immune deficiencies and disorders, infectious
CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
CC bone degenerative disorders, or periodontal disease, and for gut
CC protection or regeneration and treatment of lung or liver fibrosis.
CC reperfusion injury in various tissues and conditions resulting from
CC systemic cytokine damage.
CC N.B. The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 103 AA;

Query Match 5.0%; Score 7; DB 23; Length 103;
Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 29 LLRVKSS 35
Db 10 LLRVKSS 16
|||||

RESULT 7
AAO10778
ID AAO10778 standard; Protein; 141 AA.
XX
AC AAO10778;
DT
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 24670.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.

XX Homo sapiens.
OS
XX WO200164835-A2.
PN
XX
PD 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US04927.
PF
XX 28-FEB-2000; 2000US-0515126.
PR
PR 18-MAY-2000; 2000US-0577409.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
PI Tang YT, Liu C, Drmanac RT;
XX
XX WPI; 2001-514838/56.
DR
DR N-PSDB; AA190709.

XX Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
XX Claim 20; SEQ ID NO 24670; 1399pp + Sequence Listing; English.

XX The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to

CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 141 AA;

Query Match 5.0%; Score 7; DB 22; Length 141;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 132 LKSQGVN 138
Db 24 LKSQGVN 30
|||||

RESULT 8
ABP31776
ID ABP31776 standard; Protein; 157 AA.
XX
AC ABP31776;
DT
DT 08-JUL-2002 (first entry)
XX
DE Human ORP749 protein, SEQ ID NO:1498.

XX Human; ORP; open reading frame; ORFX; drug screening; diagnosis;
KW disease monitoring; cytokine; cell proliferation; cell differentiation;
KW immune modulation; haematopoiesis regulation; tissue growth;
KW angiogenesis; activin; inhibin; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; tumour inhibition; bodily characteristic; fertility;
KW behaviour; cancer; proliferative disorder; neurological disorder;
KW cardiovascular disease; immune system disorder; organ transplantation;
KW tissue growth disorder; tissue regeneration disorder; diabetes mellitus;
KW hypothyroidism; cholesterol ester storage disease; infection; vulnery;
KW vasotrophic; antipsoriatic; antidiabetic; cytostatic; neurotropic;
KW neuroprotective; antithrombotic; anticoagulant; thrombolytic;
KW cardiant; hypotensive; antithyroid; antiinflammatory; immunomodulator;
KW dermatological; analgesic; virucide; antibacterial; fungicide.

XX Homo sapiens.
OS
XX WO200190366-A2.
PN
XX
PD 29-NOV-2001.
XX
XX 24-MAY-2001; 2001WO-US17076.
PF
XX 24-MAY-2000; 2000US-206690P.
PR
XX (CURA-) CURAGEN CORP.
PA
XX
PI Leach MD, Shinkets RA;
XX
XX WPI; 2002-106200/14.
DR
DR N-PSDB; ABN/5802.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
PT preventing and treating cardiovascular disease, neurodegenerative,
PT hyperproliferative disorders and disorders related to organ
PT transplantation -
XX
XX Claim 10; Page 640; 2508pp; English.

XX Sequences ABP31028-ABP35561 represent 4534 novel human proteins

designated ORF (open reading frame) 1-4534, and sequences ABN75054-ABN7587 represent cDNAs encoding them. The invention also encompasses polypeptides at least 80% identical to the ORF1-ORF4534 (collectively referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic acid sequences, vectors and host cells comprising ORFX polynucleotides, the recombinant production of ORFX proteins, antibodies specific for ORFX proteins, methods of detecting ORFX polynucleotides and polypeptides, methods of screening individuals for a predisposition to an ORFX-associated disorder. The ORFX proteins of the invention have a wide range of biological activities, such as cytokine, cell proliferation, cell differentiation, immune modulation, haematopoiesis regulation, tissue growth, angiogenesis, activin or inhibin activity, chemotactic/chemokinetic activity, haemostatic activity, thrombolytic activity, receptor/ligand, antiinflammatory activity, tumour inhibition activity, and antifertile activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, nucleic acids and antibodies may be used in the treatment of cancers, other proliferative disorders such as psoriasis and benign tumours, neurological disorders such as epilepsy and Alzheimer's disease, cardiovascular diseases, immune system disorders, disorders related to organ transplantation, disorders of tissue growth and regeneration, diseases such as diabetes mellitus, hypothyroidism, and cholesterol storage disease, and infectious diseases caused by viral, bacterial, fungal and other pathogens. ORFX nucleic acids may also be used as a source of primers and probes, in the detection of ORFX genomic sequences or transcripts, in the identification and cloning of homologous sequences, in genetic diagnosis, and in forensic biology. The ORFX nucleic acids may additionally be used to produce transgenic animals which may be useful for studying the function and/or activity of ORFX protein, and in drug screening. The ORFX proteins may also be used as immunogens to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases.

XX Sequence 157 AA;

Query Match 5.0%; Score 7; DB 23; Length 157;
 Best Local Similarity 100.0%; Pred. No. 63;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 LRLSKSQ 135
 DB 132 LRLSKSQ 138
 |||||

RESULT 9

ID ABB68671 standard; Protein; 159 AA.

XX ABB68671;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 32805.

XX Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

XX 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

DR WPI; 2001-656860/75.
 DR N-PSDB; ABL12774.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
 PT interactions -
 PT interactions -
 XX Disclosure; SEQ ID NO 32805; 21pp + Sequence Listing; English.
 XX The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 159 AA;

Query Match 5.0%; Score 7; DB 22; Length 159;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ESTSTTT 8
 |||||
 DB 29 ESTSTTT 35

RESULT 10

ID AAU41908 standard; Protein; 202 AA.

XX AAU41908;

XX 13-FEB-2002 (first entry)

XX Propionibacterium acnes immunogenic protein #2804.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181591-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US12865.

XX 21-APR-2000; 2000US-199047P.

XX 02-JUN-2000; 2000US-208841P.

XX 07-JUL-2000; 2000US-216747P.

XX (CORI-) CORIXA CORP.

XX Sksiky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;

XX L'maisonneuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

XX N-PSDB; AAS59515.

XX Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris -
 XX Example 1; SEQ ID No 3103; 1069pp; English.

CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
CC polypeptides. The proteins and their associated DNA sequences are used in
CC the treatment, prevention and diagnosis of medical conditions caused by
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
CC pustulosis, hyperostosis and osteomyelitis), uveitis and endophthalmitis.
CC P. acnes is also involved in infections of bone, joints and the central
CC nervous system, however it is particularly involved in the inflammatory
CC lesions associated with acne vulgaris. A method for detecting the
CC presence or absence of P. acnes in a patient comprises contacting a
CC sample with a binding agent that binds to the proteins of the invention
CC and determining the amount of bound protein in the sample. The
CC polypeptides may be used as antigens in the production of antibodies
CC specific for P. acnes proteins. These antibodies can be used to
CC downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA).
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 202 AA;

Query Match 5.0%; Score 7; DB 22; Length 202;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 CGHRVLP 54
Db 125 CGHRVLP 131
|||||

RESULT 11
ABB67442
ID ABB67442 standard; Protein; 203 AA.

XX ABB67442;
AC ABB67442;
XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 29118.
DE Drosophila; developmental biology; cell signalling; insecticide;
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.

XX Drosophila melanogaster.
OS WO200171042-A2.
XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.
PA Venter JC, Adams M, Li PWD, Myers EW;

PI WPI; 2001-656860/75.
XX N-PSDB; ABL11545.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PT

XX Disclosure; SEQ ID NO 29118; 21pp + Sequence Listing; English.
XX

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 203 AA;
Query Match 5.0%; Score 7; DB 22; Length 203;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 LLRVKSS 35
Db 192 LLRVKSS 198
|||||

RESULT 12
AAB86467
ID AAB86467 standard; Protein; 214 AA.

XX AAB86467;
AC AAB86467;
XX 26-OCT-2001 (first entry)

XX Crypthecodinium sp elongase protein fragment from clone Cc_PSE1.
DE Elongase; plant; transgenic plant; fatty acid; PUFA; oil; lipid; food;
KW polyunsaturated fatty acid; fodder; cosmetic; pharmaceutical.

XX Crypthecodinium sp.
OS WO200159128-A2.
XX 16-AUG-2001.

XX 08-FEB-2001; 2001WO-EP01346.
XX 09-FEB-2000; 2000DE-1005973.
PR 17-MAY-2000; 2000DE-1023893.

XX 19-DEC-2000; 2000DE-1063387.
XX (BADI) BASF AG.
XX Heinz E, Zank T, Zaehrer U, Lerchl J, Renz A;

XX WPI; 2001-529842/58.
XX N-PSDB; AAB48739.

XX New elongase gene extends 16, 18 and 20 carbon fatty acids, useful to
PT manipulate plants to produce polyunsaturated fatty acids for the
PT foodstuffs, cosmetics and pharmaceutical industries -
XX

XX Claim 2c; Page 129-130; 135pp; German.
XX

XX This invention describes a novel isolated nucleic acid from a plant or
CC algae which encodes a polypeptide which extends a C₁₆, C₁₈ or C₂₀
CC fatty acid having at least two double bonds by at least two carbon atoms.
CC The products of the invention can be used to produce polyunsaturated
CC fatty acids (PUFAs) in the form of oils, lipids or fatty acids in a
CC method which comprises breeding organisms e.g. transgenic plants
CC containing the above nucleic acids, constructs or vectors encoding a
CC polypeptide which extends a C₁₆, C₁₈ or C₂₀ fatty acid having at
CC least two double bonds by at least two carbon atoms, under PUFA forming
CC conditions. The oils, lipids or fatty acid compositions produced by the
CC invention are used in fodder, food, cosmetics and pharmaceuticals. The
CC invention is more efficient at producing polyunsaturated fatty acids in a
CC broad spectrum of plants than prior art. This sequence represents the
CC Crypthecodinium sp. elongase protein isolated from clone Cc_PSE1 which
CC is described in the method of the invention.

3Q Sequence 214 AA;

Query Match 5.0%; Score 7; DB 22; Length 214;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2Y 88 RELSRKI 94
|||||
3b 192 RELSRKI 198

RESULT 13
ABG26750
ID ABG26750 standard; Protein; 236 AA.

AC ABG26750;
CX
CX 18-FEB-2002 (first entry)
CX
CX Novel human diagnostic protein #26741.
CX Human; chromosome mapping; gene mapping; gene therapy; forensic;
CX food supplement; medical imaging; diagnostic; genetic disorder.

CX Homo sapiens.

CX WO2001175067-A2.
CX
CX 11-OCT-2001.
CX
CX 30-MAR-2001; 2001WO-US088631.
CX
CX 31-MAR-2000; 2000US-0540217.
CX 23-AUG-2000; 2000US-0649167.
CX
CX (HYSE-) HYSEQ INC.

CX Drmanac RT, Liu C, Tang YT;

CX WPI; 2001-639362/73.
CX N-PSDB; AAS90937.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -

CX Claim 20; SEQ ID No 57109; 103pp; English.

CX The invention relates to isolated polynucleotide (I) and
CX polypeptide (II) sequences. (I) is useful as hybridisation probes,
CX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CX and gene mapping, and in recombinant production of (II). The
CX polynucleotides are also used in diagnostics as expressed sequence tags
CX for identifying expressed genes. (I) is useful in gene therapy techniques
CX to restore normal activity of (II) or to treat disease states involving
CX (II). (II) is useful for generating antibodies against it, detecting or
CX quantitating a polypeptide in tissue, as molecular weight markers and as
CX a food supplement. (II) and its binding partners are useful in medical
CX imaging of sites expressing (II). (I) and (II) are useful for treating
CX disorders involving aberrant protein expression or biological activity.
CX The polypeptide and polynucleotide sequences have applications in
CX diagnostics, forensics, gene mapping, identification of mutations
CX responsible for genetic disorders or other traits to assess biodiversity
CX and to produce other types of data and products dependent on DNA and
CX amino acid sequences. ABG00010-ABG30377 represent novel human
CX diagnostic amino acid sequences of the invention.

CX Note: The sequence data for this patent did not appear in the printed
CX specification, but was obtained in electronic format directly from WIPO
CX at ftp.wipo.int/pub/published_pct_sequences.

CX Sequence 236 AA;

Query Match 5.0%; Score 7; DB 22; Length 236;

Best Local Similarity 100.0%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 LAMLRAL 44
|||||
Db 112 LAMLRAL 118

RESULT 14
ABBI2033
ID ABBI2033 standard; peptide; 236 AA.

AC ABBI2033;
CX
CX 11-JAN-2002 (first entry)
CX
CX Human novel protein, SEQ ID NO:2403.

CX Human; cytokine; cell proliferation; cell differentiation; growth factor;
CX haematopoiesis regulation; tissue growth; immunomodulator; activin;
CX inhibit; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
CX proliferation; metastasis; cancer; tumour; haematopoietic disorder;
CX myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
CX chronic inflammatory condition; proliferative retinopathy;
CX atherosclerosis; coronary heart disease; arterial ischaemia;
CX bone disorder; osteoporosis; vascular growth disorder;
CX tissue regeneration; wound healing; infection; immune disorder;
CX cell culture; drug screening; gene therapy; antiinflammatory;
CX antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
CX cytostatic; osteopathic; vasotropic; cardiac; virucide; antibacterial;
CX antifungal; vulnery; antiulcer.

CX Homo sapiens.

CX WO200157188-A2.

CX 09-AUG-2001.

CX 05-FEB-2001; 2001WO-US03800.

CX 03-FEB-2000; 2000US-0496914.

CX 27-APR-2000; 2000US-0560875.

CX (HYSE-) HYSEQ INC.

CX Tang YT, Liu C, Drmanac RT;

CX WPI; 2001-457740/49.

CX N-PSDB; ABA09277.
PT Human proteins and DNA encoding sequences useful for preventing,
PT treating or ameliorating a medical condition in a mammalian subject
PT e.g. arthritis and cancer -

CX Claim 20; Page 300; 1963pp; English.

CX Sequences ABBI0981-ABBI2330 represent 1350 novel human polypeptides, and
CX sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CX invention also relates to vectors and recombinant host cells comprising a
CX nucleotide of the invention, methods of producing the novel polypeptides,
CX antibodies against the polypeptides, methods of detecting the nucleotides
CX or polypeptides in a sample, and methods of identifying compounds which
CX bind to polypeptides of the invention. Although novel, many of the
CX polypeptides of the invention have homology to known proteins, thereby
CX giving an insight into their probable biological activities, and hence
CX potential therapeutic applications. The polypeptides of the invention may
CX have various activities, including cytokine, cell proliferation or cell
CX differentiation activities, stem cell growth factor activity;
CX haematopoiesis regulatory activity; tissue growth activity;
CX immunomodulatory activity; activin- or inhibin-related activities;
CX chemotactic or chemokinetic activities; haemostatic, thrombotic or
CX thrombolytic activities; receptor or ligand activities; or may be

CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.
 CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC can also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention.

XX Sequence 236 AA;
 Query Match 5.0%; Score 7; DB 22; Length 236;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 PELRELS 91
 Db 6 PELRELS 14

RESULT 15
 AAM80027
 ID AAM80027 standard; Protein; 236 AA.

XX AC AAM80027;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human protein SEQ ID NO 3673.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.

XX OS Homo sapiens.
 XX FN WO200157190-A2.
 XX PD 09-AUG-2001.
 XX PF 05-FEB-2001; 2001WO-US04098.
 XX PR 03-FEB-2000; 2000US-0496914.
 XX PR 27-APR-2000; 2000US-0560875.
 XX PR 20-JUN-2000; 2000US-0598075.
 XX PR 19-JUL-2000; 2000US-0620325.
 XX PR 01-SEP-2000; 2000US-0654936.
 XX PR 15-SEP-2000; 2000US-0663561.
 XX PR 20-OCT-2000; 2000US-0693325.
 XX PR 30-NOV-2000; 2000US-0728422.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI: 2001-476283/51.
 DR N-PSDB; AAK53160.

XX Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX Claim 20; Page 410; 6221pp; English.
 XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX Sequence 236 AA;

Query Match 5.0%; Score 7; DB 22; Length 236;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 PELRELS 91
 Db 8 PELRELS 14

RESULT 16
 AAM80028
 ID AAM80028 standard; Protein; 236 AA.

XX AC AAM80028;
 XX DT 06-NOV-2001 (first entry)
 XX DE Human protein SEQ ID NO 3674.

XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorder; arthritis; inflammation.

XX OS Homo sapiens.
 XX FN WO200157190-A2.
 XX PD 09-AUG-2001.
 XX PF 05-FEB-2001; 2001WO-US04098.
 XX PR 03-FEB-2000; 2000US-0496914.
 XX PR 27-APR-2000; 2000US-0560875.
 XX PR 20-JUN-2000; 2000US-0598075.
 XX PR 19-JUL-2000; 2000US-0620325.
 XX PR 01-SEP-2000; 2000US-0654936.
 XX PR 15-SEP-2000; 2000US-0663561.
 XX PR 20-OCT-2000; 2000US-0693325.
 XX PR 30-NOV-2000; 2000US-0728422.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
 PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
 XX WPI: 2001-476283/51.
 DR N-PSDB; AAK53161.

PT Nucleic acids encoding polypeptides with cytokine-like activities,
 PT useful in diagnosis and gene therapy -
 XX
 XX Claim 20; Page 410; 6221pp; English.
 XX
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and/or
 CC activin/inhibin activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.
 XX
 XX Sequence 236 AA;

Query Match 5.0%; Score 7; DB 22; Length 236;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 PELRELS 91
 Db 8 PELRELS 14

RESULT 17
 AAM41648
 ID AAM41648 standard; Protein; 236 AA.

AC AAM41648;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 6579.

XX Human; neurotrophic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.

OS WO200153312-A1.

PN 26-JUL-2001.

PD 26-DEC-2000; 2000WO-US34263.

PF 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

DR N-PSDB; AAI60804.

XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 XX Example 2; SEQ ID NO 6579; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAW42213) with neurotropic,
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression.
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.

XX Sequence 236 AA;

Query Match 5.0%; Score 7; DB 22; Length 236;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 PELRELS 91
 Db 8 PELRELS 14

RESULT 18

AAV83184

ID AAV83184 standard; peptide; 293 AA.

XX AAV83184;

DT 24-JUL-2000 (first entry)

XX Melanocortin receptor MC4 Factor Xa cleavage product.

XX Membrane polypeptide; lipid matrix; synthesis; ligation;
 KW chemoselective ligation; fluorescence resonance energy transfer;
 KW FRET; chromophore; ligand; receptor domain; drug screening;
 KW diagnosis; ion channel; melanocortin receptor; MC4.

XX Synthetic.

OS Homo sapiens.

XX WO200012536-A2.

PN 09-MAR-2000.

PD 26-AUG-1999; 99WO-US19542.

PF 31-AUG-1998; 98US-0144964.

PR 05-MAR-1999; 99US-0263971.

XX (GRYP-) GRYPHON SCI.

XX Kochendoerfer GG, Hunter CL, Kent SBH, Botti P;

XX WPI; 2000-270792/23.

XX Selectively labeled membrane peptides, useful e.g. for detecting ligand
 PT binding to receptors and in drug screening, are prepared, in lipid
 PT matrix, by reaction between amino acid residues

XX Example 11; Page 70; 120pp; English.

CC New methods are described by which membrane polypeptides can be
CC labelled. The method comprises chemoselective chemical ligation of
CC the membrane polypeptide which is incorporated in a lipid matrix,
CC and a ligation label. Both contain an amino acid having an
CC unprotected reactive group that together undergo chemoselective
CC ligation to form a covalent bond. The method can be used to label
CC folded polypeptides embedded in a lipid membrane, by treating the
CC polypeptide with a reagent that cleaves specifically adjacent to an
CC amino acid with an unprotected reactive group, and then ligating the
CC cleaved polypeptide with the ligation label. The ligation label can
CC be a chromophore, thus ligand binding to membrane bound polypeptides
CC can be detected by contacting a membrane bound polypeptide comprising
CC a chromophore, with the ligand under investigation and screening for
CC binding in an assay characterized by detecting fluorescence resonance
CC energy transfer (FRET) between the chromophore and a second
CC chromophore, the chromophores comprising a donor and acceptor pair of
CC a resonance energy transfer system. The methods are used for lipid
CC matrix-assisted chemical ligation and synthesis of membrane
CC polypeptides. Labeled membrane polypeptides are used to detect ligand
CC binding and the identification of receptor domains, e.g. for
CC structure/activity studies. They can also be used in drug screening,
CC selection or design, and for diagnosis. The methods are particularly
CC used for fluorescent resonance energy transfer (FRET) analysis of
CC previously inaccessible membrane polypeptides. The method allows
CC site-specific incorporation of labels during polypeptide synthesis
CC and analysis of previously inaccessible membrane proteins. A
CC Melanocortin receptor MC4 which also comprises a factor Xa cleavage
CC site (AAV83182) can be cleaved with Factor Xa to give a
CC C-terminal alpha-thioester modified MC4 receptor ligation label
CC (AAV83183) and this MC4 receptor membrane polypeptide cleavage product
CC Chemical ligation of cleaved MC4 in alternative membrane patches or
CC micelles to an MC4 ligation label produces the synthetic labeled
CC MC4 product (AAV83183).

XX Sequence 293 AA;
SQ Query Match 5.0%; Score 7; DB 21; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPQTGA 58
Db 189 VLPQTGA 195
|||||

RESULT 19
ABG71866
ID ABG71866 standard; protein; 293 AA.
XX AC ABG71866;
XX DT 15-JAN-2003 (first entry)
XX DE Melanocortin receptor, MC4, factor Xa cleavage product.
XX KW Melanocortin receptor; membrane protein; MC4; factor Xa; lipid matrix;
KW Chemoselective chemical ligation; CCL; ligation label; ligand binding;
KW FRET; fluorescence resonance energy transfer; receptor; human.
XX OS Homo sapiens.
XX PN US6451543-B1.
XX PD 17-SEP-2002.
XX PF 26-AUG-1999; 99US-0384302.
XX PR 31-AUG-1998; 98US-0144964.
XX PR 05-MAR-1999; 99US-0263971.
XX PA (GRYP-) GRYPHON SCI.
XX PI Kochendoerfer GG, Hunter CL, Kent SBH, Botti P;

XX WPI; 2003-045578/04.
XX Chemoselective chemical ligation of membrane polypeptides useful for
PT assaying ligand binding to membrane polypeptides, involves covalently
PT binding polypeptides incorporated in a lipid matrix with ligation
PT labels -
XX Example 11; Column 48; 52pp; English.
XX The invention relates to chemoselective chemical ligation (CCL) of a
CC membrane polypeptide, (M1) involves contacting (under CCL conditions):
CC (a) polypeptide (I) incorporated in lipid matrix, comprising first
CC amino acid (A1) having unprotected reactive group; (b) with ligation
CC label (II) comprising second amino acid (A2) having unprotected reactive
CC group, (A2) is capable of CCL with A1, and contacting (I) with (II) causes
CC a covalent bond to be formed between unprotected reactive groups of A1
CC and A2). Also included are a composition comprising an integral membrane
CC polypeptide embedded in a lipid matrix and at least one non-naturally
CC occurring amino acid comprising a unprotected reactive group capable of
CC CCL with (II) having a compatible unprotected reactive group; and a
CC composition comprising a membrane polypeptide embedded in a lipid matrix
CC (the membrane polypeptide has at least two amino acid residues
CC covalently joined through a non-natural backbone bond). The method
CC is used for chemoselective chemical ligation of a folded membrane
CC polypeptide, or an integral or transmembrane polypeptide, where the
CC transmembrane polypeptide is a receptor. The method is useful for
CC detecting a ligand that directly or indirectly interacts with a folded
CC membrane polypeptide embedded in a lipid matrix. This
CC method is particularly useful for diagnostic assays, screening new
CC compounds for drug development, and other structural and functional
CC assays that employ binding of a ligand to a pre-folded membrane
CC polypeptide. (M1) and (II) can be used to assay ligand binding to
CC membrane polypeptides and domains comprising a receptor, and thus are
CC extremely useful for structure/function studies, drug
CC screening/selection/design and diagnostics, etc. including
CC high-throughput applications. The methods and compositions are
CC particularly suited for fluorescence resonance energy transfer (FRET)
CC analyses of previously inaccessible membrane polypeptides. The
CC present sequence is the melanocortin receptor, MC4, factor Xa
CC cleavage product, used to demonstrate the method of the invention.

XX Sequence 293 AA;
SQ Query Match 5.0%; Score 7; DB 24; Length 293;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPQTGA 58
Db 189 VLPQTGA 195
|||||

RESULT 20
AAU08750
ID AAU08750 standard; Protein; 311 AA.
XX AC AAU08750;
XX DT 28-DEC-2001 (first entry)
XX DE Human melanocortin-4 receptor (MC4R) polypeptide.
XX KW Melanocortin-4 receptor; MC4R; meat quality; drip loss; marbling; sheep;
KW pig; cow; chicken; animal breeding; pH; polymorphism; slaughter; human.
XX OS Homo sapiens.
XX PF Key Location/Qualifiers
XX FT Misc-difference 298 /label= OTHER
XX FT /note= "OTHER= any amino acid"

PN WO200175161-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 29-MAR-2001; 2001WO-US10076.
 XX
 PR 30-MAR-2000; 2000US-0538165.
 XX
 PA (IOWA) UNIV IOWA STATE RES FOUND INC.
 XX
 PI Rothschild MF, Emmett R, Kim KS;
 XX
 DR WPI; 2001-626446/72.
 XX
 PT Identifying genotype associated with good meat quality, useful e.g. for
 PT selecting animals for breeding, by detecting a polymorphism in the
 PT melanocortin-4 receptor gene -
 XX
 PS Example 1; Page 50-51; 56pp; English.
 XX
 CC The invention relates to a method for identifying an animal having a
 CC genotype that indicates good meat quality traits such as drip loss,
 CC marbling, pH and colour. This involves assaying a nucleic acid for a
 CC polymorphism in the melanocortin-4 receptor (MC4R) gene, which is
 CC associated with meat quality traits in animals. Assaying for the presence
 CC of at least one genetic marker at this gene region allows genetic
 CC evaluation. The method is used to identify meat producing animals, such
 CC as pigs, cows, sheep and chickens, with favourable meat quality traits,
 CC particularly to select animals for breeding and to ensure uniformity at
 CC slaughter. This sequence represents the human melanocortin-4 receptor.
 CC Note: The specification states that this protein is encoded by the DNA
 CC sequence featured in AAS14759.
 XX
 SQ Sequence 311 AA;
 Query Match 5.0%; Score 7; DB 22; Length 311;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 52 VLPGTGA 58
 DB 186 VLPGTGA 192
 |||||
 RESULT 21
 AAB65807
 ID AAB65807 standard; Protein; 320 AA.
 AC
 XX
 DT 27-MAR-2001 (first entry)
 XX
 DE RPPS-like protein #14.
 XX
 KW Cell death modulator; programmed cell death; PCD; apoptosis;
 KW forestry plant.
 XX
 OS Pinus radiata.
 XX
 PN WO200075331-A1.
 XX
 PD 14-DEC-2000.
 XX
 PF 02-JUN-2000; 2000WO-NZ00086.
 XX
 PR 04-JUN-1999; 99US-0325932.
 XX
 PA (GENE-) GENESIS RES & DEV CORP LTD.
 PA (FLET-) FLETCHER CHALLENGE FORESTS LTD.
 XX
 PI Flinn B, Lasham A;
 XX
 DR WPI; 2001-061724/07.

DR N-PSDB; AAF44834.
 XX
 PT Novel defender against cell death polynucleotide useful for modulating
 PT programmed cell death pathway and specific development pathways in
 PT forestry plant -
 XX
 PS Claim 22; Pages 131-132; 142pp; English.
 XX
 CC The present invention relates to coding sequences (see AAF44740-FA4840
 CC and AAF4843-F4844) and proteins (see AAB55714-B65814) involved in
 CC programmed cell death (PCD; apoptosis). The coding sequences and proteins
 CC of the present invention are useful for modulating a PCD or cell death
 CC pathway and various developmental pathways in a forestry plant, by
 CC stably incorporating one of the present coding sequences into the genome
 CC of the forestry plant, where the coding sequence provides a PCD pathway
 CC that is not present in a native form of the forestry plant.
 XX
 SQ Sequence 320 AA;
 Query Match 5.0%; Score 7; DB 22; Length 320;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 126 FRHLRSL 132
 DB 252 FRHLRSL 258
 |||||
 RESULT 22
 AAM19704
 ID AAM19704 standard; Protein; 332 AA.
 XX
 AC AAM19704;
 XX
 DT 19-AUG-1997 (first entry)
 XX
 DE Melanocortin-4 receptor.
 XX
 KW Melanocortin-3; MC3R; MC1R; MC2R; MC4R; MC5R; human; mouse; melanocyte;
 KW pro-opiomelanocortin; adrenal cortical function; behaviour; learning;
 KW memory; cardiovascular system; analgesia; thermoregulation; prolactin;
 KW neurohumoral agent; biogenic amine.
 XX
 OS Homo sapiens.
 XX
 PN US5622860-A.
 XX
 PD 22-APR-1997.
 XX
 PF 17-FEB-1994; 94US-0200711.
 XX
 PR 17-FEB-1994; 94US-0200711.
 XX
 PA (UNMI) UNIV MICHIGAN.
 XX
 PI Gantz I, Yamada T;
 XX
 DR WPI; 1997-244394/22.
 DR N-PSDB; AAT68790.
 XX
 PT Nucleic acid molecules encoding melanocortin receptors - useful to
 PT transfect mammalian cells lacking endogenous receptors to induce
 PT their expression
 XX
 PS Claim 4; Column 43-46; 58pp; English.
 XX
 CC AAM19703-W19707 represent the human and mouse melanocortin (MC)
 CC receptors. This sequence represents the MC4R, expressed primarily in
 CC brain, but absent in the adrenal cortex, melanocytes and placenta. The
 CC gene encoding this sequence is located at chromosome locus 18q21.3. MCs
 CC are products of pro-opiomelanocortin post-translational processing, and
 CC are known to have a broad array of physiological actions. MCs are known
 CC to have effects on adrenal cortical functions and on melanocytes, as well

as affecting behaviour, learning, memory, control of the cardiovascular system, analgesia, thermoregulation and the release of other neurohumoral agents (such as prolactin and biogenic amines). The nucleic acids can be used to transfect mammalian cells lacking endogenous MC receptors to induce their expression. These sequences can also be used to screen and identify drugs which specifically react with MCRs on the surface of a cell. The drugs can then be used for treating diseases which have MCRs implicated as one of their causes. Vectors containing these sequences can also be used to treat the diseases.

Query Match 5.0%; Score 7; DB 18; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPPTGA 58
DB 228 VLPPTGA 234

RESULT 23
AAW79687
ID AAW79687 standard; Protein; 332 AA.
XX AC AAW79687;
XX DT 17-DEC-1998 (first entry)
XX DE Melanocortin-4 receptor.
XX KW Human melanocortin-4 receptor; MC4; MC1; MC3; therapeutic; brain;
XX KW adrenal cortex; melanocyte; placenta.
XX OS Homo sapiens.
XX PN US5817787-A.
XX PD 06-OCT-1998.
XX PF 23-APR-1997; 97US-0842045.
XX PR 17-FEB-1994; 94US-0200711.
XX PR 27-JUN-1996; 96US-0672109.
XX PR 23-APR-1997; 97US-0842045.
XX PA (UNMI) UNIV MICHIGAN.
XX PI Gantz I, Yamada T;
XX DR WPI; 1998-556471/47.
XX DR N-PSDB; AAV62352.
XX PT DNA encoding melanocortin-5 receptor - useful in hybridisation
XX PT assays for melanocortin-5 receptor nucleic acids
XX PS Disclosure; Column 43-46; 58pp; English.

The present sequence represents the human melanocortin-4 (MC4) receptor, the gene of which has been localised to chromosome 18q21.3. This receptor is activated by both the amino and carboxyl terminal end amino acids of melanocortins and has been found to be expressed primarily in the brain and is absent from the adrenal cortex, melanocytes and placenta. The DNA sequence that produces this polypeptide was identified by using oligonucleotides constructed from previously identified receptors MC1 and MC3, this was performed by using these oligonucleotides to search genomic DNA for other members of the receptor family. These genes and their products may be used to provide therapeutic vehicles for the treatment of processes involving the function of melanocortin receptors.

Query Match 5.0%; Score 7; DB 18; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPPTGA 58
DB 228 VLPPTGA 234

RESULT 23
AAW79687
ID AAW79687 standard; Protein; 332 AA.
XX AC AAW79687;
XX DT 17-DEC-1998 (first entry)
XX DE Melanocortin-4 receptor.
XX KW Human melanocortin-4 receptor; MC4; MC1; MC3; therapeutic; brain;
XX KW adrenal cortex; melanocyte; placenta.
XX OS Homo sapiens.
XX PN US5817787-A.
XX PD 06-OCT-1998.
XX PF 23-APR-1997; 97US-0842045.
XX PR 17-FEB-1994; 94US-0200711.
XX PR 27-JUN-1996; 96US-0672109.
XX PR 23-APR-1997; 97US-0842045.
XX PA (UNMI) UNIV MICHIGAN.
XX PI Gantz I, Yamada T;
XX DR WPI; 1998-556471/47.
XX DR N-PSDB; AAV62352.
XX PT DNA encoding melanocortin-5 receptor - useful in hybridisation
XX PT assays for melanocortin-5 receptor nucleic acids
XX PS Disclosure; Column 43-46; 58pp; English.

Query Match 5.0%; Score 7; DB 19; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPPTGA 58
DB 228 VLPPTGA 234

RESULT 24
AAW37831
ID AAW37831 standard; Protein; 332 AA.
XX AC AAW37831;
XX DT 28-JUL-1998 (first entry)
XX DE Human melanocortin-4 receptor.
XX KW Human melanocortin-4 receptor gene; metabolic disorder; agonist;
XX KW antagonist; feeding; eating disorder; anorexia; obesity; cachexia;
XX KW cancer; inhibition; melanocortin receptor; MCR.
XX OS Homo sapiens.
XX PN W09810068-A2.
XX PD 12-MAR-1998.
XX PF 04-SEP-1997; 97WO-US15565.
XX PR 04-SEP-1996; 96US-0706281.
XX PA (UYOR-) UNIV OREGON HEALTH SCI.
XX PI Boston BA, Chen W, Cone RD, Fan W, Kesterton RA;
XX PI Lu D;
XX DR WPI; 1998-193618/17.
XX DR N-PSDB; AAV19142.
XX PT Identifying melanocortin receptor agonists and antagonists - using a
XX PT panel of recombinant mammalian cells expressing alpha-melanocyte
XX PT stimulating hormone, ACTH, MC-3, MC-4 and MC-5 receptors
XX PS Example 2F; Fig 6A-B; 121pp; English.

This is the amino acid sequence of the human melanocortin-4 receptor (MCR-4). The MCR agonists and antagonists can be used for modifying feeding behaviour in an animal. The antagonists can be used for stimulating feeding while the agonists can be used for inhibiting feeding. They can be used for the treatment of eating disorders such as anorexia and obesity, and other pathological weight and eating-related disorders. They can also be used to treat failure to thrive disorders and disease-related cachexia, such as occurs in cancer patients, as well as other metabolic disorders.

Query Match 5.0%; Score 7; DB 19; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPPTGA 58
DB 228 VLPPTGA 234

RESULT 25
AAW42377
ID AAW42377 standard; Protein; 332 AA.
XX AC AAW42377;

XX 25-MAR-2003 (updated)
 DT 08-JUN-1998 (first entry)
 DT
 XX Homo sapiens mutant melanocortin 4 receptor Ile137Thr.
 DE
 XX Melanocortin 4 receptor; MC4-R gene; body weight disorder;
 KW treatment; obesity; anorexia; cachexia; Ile137Thr; mutant.
 XX
 XX Homo sapiens.
 DS
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 137..137
 FT /note= "Ile137Thr mutation from wild-type"
 XX
 XX WO9747316-A1.
 PN 18-DEC-1997.
 PD
 XX 09-JUN-1997; 97WO-US09969.
 PF
 XX 10-JUN-1996; 96US-0662560.
 PR 08-JAN-1997; 97US-0780749.
 PR 06-JUN-1997; 97US-0870511.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX Gu W, Huszar D, Lee F;
 PI WPI; 1998-052026/05.
 XX N-PSDB; AAV03251.
 DR
 XX Drug screening assays to identify compounds for body weight disorder
 PT treatment - e.g. obesity, anorexia and cachexia, using melanocortin
 PT 4 receptor as target
 XX
 XX Disclosure; Fig 11; 11lpp; English.
 PS
 XX The sequence is that of a mutant melanocortin 4 receptor (MC4-R).
 CC the mutation is the Ile137Thr mutation. The sequence can be used in the
 CC generation of drug screening assays to identify compounds which could
 CC be used in the treatment of body weight disorders e.g. obesity, anorexia
 CC and cachexia. Specific compounds include agonists or antibodies that
 CC bind and activate the MC4-R to induce weight loss, an antibody or
 CC extracellular domain of the MC4-R that inhibits MC4-R activation and
 CC therefore induces weight gain or an oligonucleotide that inhibits
 CC translation by encoding an antisense or ribozyme molecule that targets
 CC MC4-R transcripts or by forming a triple helix with the MC4-R gene
 CC promoter to induce weight gain.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 332 AA;
 Query Match 5.0%; Score 7; DB 19; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 52 VLPQTGA 58
 DB 228 VLPQTGA 234
 |||||
 RESULT 26
 ID AAW42378 standard; Protein; 332 AA.
 AC AAW42378;
 XX
 XX 25-MAR-2003 (updated)
 DT 08-JUN-1998 (first entry)
 DT
 XX Homo sapiens mutant melanocortin 4 receptor Vall02Ile.
 DE
 XX

KW Melanocortin 4 receptor; MC4-R gene; body weight disorder;
 KW treatment; obesity; anorexia; cachexia; Vall02Ile; mutant.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 102..102
 FT /note= "Vall02Ile mutation from wild-type"
 XX
 XX WO9747316-A1.
 PN 18-DEC-1997.
 PD
 XX 09-JUN-1997; 97WO-US09969.
 PF
 XX 10-JUN-1996; 96US-0662560.
 PR 08-JAN-1997; 97US-0780749.
 PR 06-JUN-1997; 97US-0870511.
 XX
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX Gu W, Huszar D, Lee F;
 PI WPI; 1998-052026/05.
 XX N-PSDB; AAV03252.
 DR
 XX Drug screening assays to identify compounds for body weight disorder
 PT treatment - e.g. obesity, anorexia and cachexia, using melanocortin
 PT 4 receptor as target
 XX
 XX Disclosure; Fig 12; 11lpp; English.
 PS
 XX The sequence is that of a mutant melanocortin 4 receptor (MC4-R).
 CC the mutation is the Vall02Ile mutation. The sequence can be used in the
 CC generation of drug screening assays to identify compounds which could
 CC be used in the treatment of body weight disorders e.g. obesity, anorexia
 CC and cachexia. Specific compounds include agonists or antibodies that
 CC bind and activate the MC4-R to induce weight loss, an antibody or
 CC extracellular domain of the MC4-R that inhibits MC4-R activation and
 CC therefore induces weight gain or an oligonucleotide that inhibits
 CC translation by encoding an antisense or ribozyme molecule that targets
 CC MC4-R transcripts or by forming a triple helix with the MC4-R gene
 CC promoter to induce weight gain.
 CC (Updated on 25-MAR-2003 to correct PR field.)
 XX
 SQ Sequence 332 AA;
 Query Match 5.0%; Score 7; DB 19; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 52 VLPQTGA 58
 DB 228 VLPQTGA 234
 |||||
 RESULT 27
 ID AAW42379 standard; Protein; 332 AA.
 AC AAW42379;
 XX
 XX 25-MAR-2003 (updated)
 DT 08-JUN-1998 (first entry)
 DT
 XX Homo sapiens mutant melanocortin 4 receptor Thr112Met.
 DE
 KW Melanocortin 4 receptor; MC4-R gene; body weight disorder;
 KW treatment; obesity; anorexia; cachexia; Thr112Met; mutant.
 XX
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers

FT Misc-difference 112..112
 FT /note= "Thr112Met mutation from wild-type"

PN WC9747316-A1.
 XX 18-DEC-1997.
 XX 09-JUN-1997; 97WO-US09969.
 XX 10-JUN-1996; 96US-0662560.
 PR 08-JAN-1997; 97US-0780749.
 PR 06-JUN-1997; 97US-0870511.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Gu W, Huszar D, Lee F;
 XX WPI; 1998-052026/05.
 DR N-PSDB; AAW42379.
 XX Drug screening assays to identify compounds for body weight disorder
 PT treatment - e.g. obesity, anorexia and cachexia, using melanocortin
 PT 4 receptor as target
 XX Disclosure; Fig 13; 11lpp; English.

XX The sequence is that of a mutant melanocortin 4 receptor (MC4-R),
 CC the mutation is the Thr112Met mutation. The sequence can be used in the
 CC generation of drug screening assays to identify compounds which could
 CC be used in the treatment of body weight disorders e.g. obesity, anorexia
 CC and cachexia. Specific compounds include agonists or antibodies that
 CC bind and activate the MC4-R to induce weight loss, an antibody or
 CC extracellular domain of the MC4-R that inhibits MC4-R activation and
 CC therefore induces weight gain or an oligonucleotide that inhibits
 CC translation by encoding an antisense or ribozyme molecule that targets
 CC MC4-R transcripts or by forming a triple helix with the MC4-R gene
 CC promoter to induce weight gain.
 CC (Updated on 25-MAR-2003 to correct PR field.)

XX Sequence 332 AA;
 SQ Query Match 5.0%; Score 7; DB 19; Length 332;
 KW Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPQTGA 58
 DB 228 VLPQTGA 234

RESULT 28
 AAW33724
 ID AAW33724 standard; Protein; 332 AA.
 XX AAW33724;
 XX 30-APR-1998 (first entry)
 XX Human melanocortin-4 (MC4) receptor.
 DE Melanocortin receptor; ligand; MC4; human.

XX Homo sapiens.
 OS US5703220-A.
 XX 30-DEC-1997.
 XX 27-JUN-1996; 96US-0671525.
 XX 17-FEB-1994; 94US-0200711.
 PR 27-JUN-1996; 96US-0671525.
 XX

PA (UNMI) UNIV MICHIGAN.
 XX Gantz I, Yamada T;
 XX WPI; 1998-076484/07.
 DR N-PSDB; AAV06400.
 XX DNA encoding human melanocortin-4 receptor - and cells useful in
 PT assay for MC4 receptor ligands

XX Claim 1; Columns 43-46; 59pp; English.

XX This is a human melanocortin receptor-4 (MC4). The MC4 receptor of this
 CC invention is activated by amino acids in the carboxyl and amino terminal
 CC portions of the heptapeptide sequence shared by all the melanocortin
 CC peptides. MC4 is expressed primarily in brain and is notably absent in
 CC the adrenal cortex, melanocytes and placenta. The MC4 receptor gene was
 CC localised to chromosome loci 18q21.3. The invention provides methods to
 CC identify ligands that bind to MC4 receptor.

SQ Sequence 332 AA;
 Query Match 5.0%; Score 7; DB 19; Length 332;
 KW Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPQTGA 58
 DB 228 VLPQTGA 234

RESULT 29
 AAY17866
 ID AAY17866 standard; Protein; 332 AA.
 XX AAY17866;
 XX 17-AUG-1999 (first entry)

XX Sulfolobus solfataricus endo-beta-1,4-glucanase CelB.
 XX Sulfolobus solfataricus; endoglucanase; CelA; CelB;
 KW endo-beta-1,4-glucanase.
 XX Sulfolobus solfataricus.

XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /label= signal
 FT Protein 22..332
 FT /label= CelB

XX DK9900097-A.
 XX 12-JAN-1999.
 XX 12-JAN-1999; 99DK-0000097.
 XX 12-JAN-1999; 99DK-0000097.
 XX (NOVO) NOVO-NORDISK AS.

XX WPI; 1999-279376/24.
 DR N-PSDB; AAX80188.

XX Novel endonuclease - produced by Sulfolobus solfataricus
 PT Claim 1; Page 31-32; 36pp; English.

XX The present sequence represents a Sulfolobus solfataricus endoglucanase,
 CC specifically endo-beta-1,4-glucanase, designated CelB. The new
 CC endo-beta-1,4-glucanase is produced by Sulfolobus solfataricus
 CC ATCC 35092.

XX SQ Sequence 332 AA;
 Query Match 5.0%; Score 7; DB 20; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 STSTTN 9
 DB 45 STSTTN 51
 |||||

RESULT 30
 AAW87869
 ID AAW87869 standard; Protein; 332 AA.
 AC AAW87869;
 DT 26-APR-1999 (first entry)
 DE Human melanocortin receptor MC4-R.
 KW Melanocortin receptor; MC4-R; human; acne; therapy;
 KW G-protein coupled receptor.
 XX Homo sapiens.
 XX WO9856914-A1.
 XX PD 17-DEC-1998.
 XX PF 12-JUN-1998; 98WO-US12098.
 XX PR 13-JUN-1997; 97US-0050063.
 XX PA (UYOR-) UNIV OREGON HEALTH SCI.
 XX PI Chen W, Cone RD, Low MJ;
 XX WPI; 1999-080902/07.
 XX DR N-PSDB; AAV63707.
 XX Identifying compounds that bind to melanocortin receptors - such as
 XX therapeutic agents for treating exocrine disorders like acne
 XX Example 2F; Page 71-73; 14pp; English.

XX This is the amino acid sequence of human melanocortin receptor
 CC MC4-R, as deduced from the nucleotide sequence of an isolated
 CC genomic DNA clone (see AAV63707). MC4-R is a G-protein coupled
 CC receptor. The invention relates to the cloning, expression and
 CC functional characterisation of mammalian melanocortin receptor
 CC MC1-R, MC2-R, MC3-R, MC4-R and MC5-R nucleic acids (see AAV63702-08)
 CC and polypeptides (see AAW87864-70), as well as expression constructs,
 CC eukaryotic cells transformed with such constructs, knockout
 CC animals, and methods and reagents for developing agonists and
 CC antagonists specific for mammalian melanocortin receptors. Such
 CC compounds, particularly those specific for MC5-R, are used to treat
 CC disorders of exocrine gland function, e.g. of the lacrimal or
 CC sebaceous glands, particularly acne, other skin disorders and 'dry
 CC eye', also disorders related to oestrus, mating, gestation and
 CC other pheromone-related conditions.

XX SQ Sequence 332 AA;
 Query Match 5.0%; Score 7; DB 20; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
 DB 228 VLPGTGA 234
 |||||

RESULT 31
 AAW92442
 ID AAW92442 standard; Protein; 332 AA.
 XX AAW92442;
 XX 21-APR-1999 (first entry)
 DT Human MC4 protein.
 DE Melanocortin-4 receptor; MC1; MC2; MC3; MC4; MC5; detection; probe;
 KW receptor binding; secondary signalling; tissue distribution.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT Protein 1..332
 FT /note= "No stop codon given"
 XX US5869257-A.
 XX PD 09-FEB-1999.
 XX PF 23-APR-1997; 97US-0842238.
 XX PR 17-FEB-1994; 94US-0200711.
 XX PR 27-JUN-1996; 96US-0671525.
 XX PR 23-APR-1997; 97US-0842238.
 XX PA (UNMI) UNIV MICHIGAN.
 XX Gantz I, Yamada T;
 XX WPI; 1999-152760/13.
 XX DR N-PSDB; AAX01964.
 XX Probe for detecting melanocortin-4 receptor genes - that
 XX specifically hybridises to defined DNA sequence
 XX Example 1; Column 45-46; 60pp; English.

XX This sequence represents the human melanocortin-4 receptor, MC4. This
 CC protein is used in a method in which a nucleic acid probe useful for
 CC specifically detecting melanocortin-4 receptor genes is described.
 CC This probe is used to isolate genes encoding melanocortin receptors,
 CC to characterise melanocortin receptor binding and secondary signalling
 CC and to determine tissue distribution of the melanocortin receptors.

XX SQ Sequence 332 AA;
 Query Match 5.0%; Score 7; DB 20; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
 DB 228 VLPGTGA 234
 |||||

RESULT 32
 AAB18769
 ID AAB18769 standard; Protein; 332 AA.
 XX AAB18769;
 XX 22-JAN-2001 (first entry)
 DE A human melanocortin-4 receptor polypeptide.
 KW Human; melanocortin-1 receptor; melanocortin-2 receptor; 16q24.3;
 KW 18p11.2; melanocortin-3 receptor; 20q13.2; melanocortin-4 receptor;
 KW 18q21.3; melanocortin.

XX OS Homo sapiens.
XX US6117975-A.
XX PD 12-SEP-2000.
XX 23-JUL-1996; 96US-0629335.
XX 17-FEB-1994; 94US-0200711.
XX (UNMI) UNIV MICHIGAN.
XX Gantz I, Yamada T;
XX WPI; 2000-610853/58.
XX N-PSDB; AAA75829.
XX New melanocortin receptor polypeptides MC3 and MC4, and genes encoding
XX the receptors, useful for providing therapeutic vehicles employed in
XX treating disorders involving melanocortin receptor function -
XX Claim 5; Column 45-48; 59pp; English.
XX The present sequence represents human melanocortin receptor polypeptide.
XX Melanocortin-1 and melanocortin-2 receptor genes have been localised to
XX Chromosome 16q24.3 and 18p11.2, respectively. The melanocortin-3 receptor
XX gene has been localised to chromosome loci 20q13.2-q13.3. The
XX melanocortin-4 receptor has been localised to chromosome 18q21.3. The
XX melanocortin-3 receptor is activated primarily by the core heptapeptide
XX sequence of melanocortins, with an adjacent terminal tyrosine being
XX required for full activation. The melanocortin receptors and their
XX respective genes are useful in providing therapeutic vehicles for the
XX treatment of processes involving the function of melanocortin receptors.
XX The genes encoding the melanocortin receptors are useful for transfecting
XX mammalian cells lacking endogenous melanocortin receptors to induce
XX expression.
XX Sequence 332 AA;
XX Query Match 5.0%; Score 7; DB 21; Length 332;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02; Indels 0; Gaps 0;
XX Matches 7; Conservative 0; Mismatches 0;
XX QY 52 VLPGTGA 58
XX 228 VLPGTGA 234
XX DE Human G protein coupled receptor MC4 protein SEQ ID NO:74.
XX Human; G protein coupled receptor; GPCR; transmembrane receptor;
XX identification; agonist; screening; therapeutic; pharmaceutical;
XX mutant.
XX Homo sapiens.
XX WO200022131-A2.
XX 20-APR-2000.
XX 13-OCT-1999; 99WO-US24065.
XX 13-OCT-1998; 98US-0170496.
XX 12-NOV-1998; 98US-0108029.

PR 20-NOV-1998; 98US-0109213.
PR 27-NOV-1998; 98US-0110060.
PR 16-FEB-1999; 99US-0120416.
PR 26-FEB-1999; 99US-0121852.
PR 12-MAR-1999; 99US-0123944.
PR 12-MAR-1999; 99US-0123945.
PR 12-MAR-1999; 99US-0123946.
PR 12-MAR-1999; 99US-0123948.
PR 12-MAR-1999; 99US-0123949.
PR 12-MAR-1999; 99US-0123951.
PR 28-MAY-1999; 99US-0136436.
PR 28-MAY-1999; 99US-0136437.
PR 28-MAY-1999; 99US-0136439.
PR 28-MAY-1999; 99US-0137127.
PR 28-MAY-1999; 99US-0137131.
PR 28-MAY-1999; 99US-0137567.
PR 30-JUN-1999; 99US-0141448.
PR 27-AUG-1999; 99US-0151114.
PR 03-SEP-1999; 99US-0152524.
PR 29-SEP-1999; 99US-0156833.
PR 29-SEP-1999; 99US-0156855.
PR 29-SEP-1999; 99US-0156634.
XX (AREN-) ARENA PHARM INC.
XX Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
XX Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX WPI; 2000-317986/27.
XX N-PSDB; AAA46069.
XX Non-endogenous, human G protein-coupled receptors for screening
XX receptor, inverse or partial agonists useful as therapeutic agents -
XX Example 1; Page 133-134; 187pp; English.
XX The present invention describes transmembrane receptors, preferably
XX human G protein coupled receptors (GPCR), for which the endogenous
XX ligand is unknown (orphan GPCR receptors). More specifically the present
XX invention relates to non-endogenous, constitutively activated versions
XX of a human GPCR. These non-endogenous human GPCRs can be useful for
XX the direct identification of candidate compounds as receptors agonists,
XX inverse agonists or partial agonists for use as pharmaceutical agents.
XX AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
XX the exemplification of the present invention.
XX Sequence 332 AA;
XX Query Match 5.0%; Score 7; DB 21; Length 332;
XX Best Local Similarity 100.0%; Pred. No. 1.3e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 52 VLPGTGA 58
XX 228 VLPGTGA 234
XX DE Human G protein coupled receptor hMC4 (A244K) protein SEQ ID NO:136.
XX Human; G protein coupled receptor; GPCR; transmembrane receptor;
XX identification; agonist; screening; therapeutic; pharmaceutical;
XX mutant.
XX Homo sapiens.
XX OS Synthetic.

XX PN WO2000022131-A2.
XX PD 20-APR-2000.
XX PP 13-OCT-1999; 99WO-US24065.
XX PR 13-OCT-1998; 98US-0170496.
XX PR 12-NOV-1998; 98US-0108029.
XX PR 20-NOV-1998; 98US-0109213.
XX PR 27-NOV-1998; 98US-0110060.
XX PR 16-FEB-1999; 99US-0120416.
XX PR 26-FEB-1999; 99US-0121852.
XX PR 12-MAR-1999; 99US-0123944.
XX PR 12-MAR-1999; 99US-0123945.
XX PR 12-MAR-1999; 99US-0123946.
XX PR 12-MAR-1999; 99US-0123948.
XX PR 12-MAR-1999; 99US-0123949.
XX PR 12-MAR-1999; 99US-0123951.
XX PR 12-MAR-1999; 99US-0136436.
XX PR 28-MAY-1999; 99US-0136437.
XX PR 28-MAY-1999; 99US-0136439.
XX PR 28-MAY-1999; 99US-0137127.
XX PR 28-MAY-1999; 99US-0137131.
XX PR 28-MAY-1999; 99US-0137567.
XX PR 30-JUN-1999; 99US-0141448.
XX PR 27-AUG-1999; 99US-0151114.
XX PR 03-SEP-1999; 99US-0152524.
XX PR 29-SEP-1999; 99US-0156633.
XX PR 29-SEP-1999; 99US-0156555.
XX PR 29-SEP-1999; 99US-0156634.
XX PR (AREN-) ARENA PHARM INC.
XX PI Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
XX PI Gore M, Liaw CW, Lin I, Lowitz K, White C;
XX PR WPI: 2000-317986/27.
XX DR N-PSDB; AAA46119.
XX DR Non-endogenous, human G protein-coupled receptors for screening
XX PT receptor, inverse or partial agonists useful as therapeutic agents -
XX PS Example 2; Page 176-177; 187pp; English.
XX CC The present invention describes transmembrane receptors, preferably
XX CC human G protein coupled receptors (GPCR), for which the endogenous
XX CC ligand is unknown (orphan GPCR receptors). More specifically the present
XX CC invention relates to non-endogenous, constitutively activated versions
XX CC of a human GPCR. These non-endogenous human GPCRs can be useful for
XX CC the direct identification of candidate compounds as receptors agonists,
XX CC inverse agonists or partial agonists for use as pharmaceutical agents,
XX CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
XX CC the exemplification of the present invention.
XX SQ Sequence 332 AA;
Query Match 5.0%; Score 7; DB 21; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
2y 52 VLPGTGA 58
|||
Db 228 VLPGTGA 234
RESULT 35
AAY94301
ID AAY94301 standard; Protein; 332 AA.
XX AC AAY94301;
XX CX
XX JT 04-AUG-2000 (first entry)

XX DE Rhesus monkey melanocortin-4 receptor protein.
XX KW Rhesus monkey; rhodopsin; G-protein coupled receptor; anorectic;
XX KW melanocyte stimulating hormone; melanocortin receptor; obesity.
XX OS Macaca mulatta.
XX XX WO200027863-A1.
XX PD 18-MAY-2000.
XX XX 05-NOV-1999; 99WO-US25767.
XX XX 09-NOV-1998; 98US-0107721.
XX XX (MERI) MERCK & CO INC.
XX XX MacNeil DJ, Weinberg DH, Van Der Ploeg LHT;
XX XX WPI: 2000-376480/32.
XX DR N-PSDB; AAA26972.
XX XX Novel DNA encoding rhesus monkey melanocortin 4 receptor protein,
XX PT recombinant vectors and host cells, useful in methods for identifying
XX PT selective agonists and antagonists -
XX PS Claim 27; Page 35; 53pp; English.
XX CC The present sequence is the rhesus monkey melanocortin-4
XX CC receptor protein (MC-4R). Melanocortin receptors belong to the rhodopsin
XX CC sub-family of G-protein coupled receptors. They bind and are
XX CC activated by peptides such as alpha-, beta-, or gamma-melanocyte
XX CC stimulating hormones derived from the pro-opiomelanocortin gene and they
XX CC are believed to mediate a wide range of physiological functions.
XX CC The rhesus MC-4R gene was isolated by PCR using a series of four
XX CC oligonucleotides (AAA26973-A26976) based on the human MC-4R gene sequence
XX CC and designed to incorporate a restriction enzyme site for cloning into
XX CC the expression vector pCI-neo. The recombinant vector was transformed
XX CC into DH5a cells in preparation for DNA sequencing. The MC-4R gene
XX CC sequence (AAA26972) or a mutated form may be introduced into an
XX CC expression vector for expression in host cells. The subcellular
XX CC membrane fractions will comprise either wild-type or mutant forms of
XX CC rhesus MC-4R at enhanced levels and can be used in assays to identify
XX CC ligand binding, activators and modulators, agonists and antagonists of
XX CC MC-4R. This will allow for selection of compounds that are active for
XX CC the rhesus receptor in vitro and will allow the selection of novel
XX CC drugs to treat obesity.
XX SQ Sequence 332 AA;
Query Match 5.0%; Score 7; DB 21; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 52 VLPGTGA 58
|||
Db 228 VLPGTGA 234
RESULT 36
AAY83182
ID AAY83182 standard; protein; 332 AA.
XX AC AAY83182;
XX XX
XX DT 24-JUL-2000 (first entry)
XX XX Melanocortin receptor MC4 comprising Factor Xa cleavage site.
XX KW Membrane polypeptide; lipid matrix; synthesis; ligation;
XX KW chemoselective ligation; fluorescence resonance energy transfer;
XX KW FRET; chromophore; ligand; receptor domain; drug screening;

diagnosis; ion channel; melanocortin receptor; MC4.
Synthetic.
Homo sapiens.
WO200012536-A2.
09-MAR-2000.
26-AUG-1999; 99WO-US19542.
31-AUG-1998; 98US-0144964.
05-MAR-1999; 99US-0263971.
(GRYP-) GRYPHON SCI.
Kochendoerfer GG, Hunter CL, Kent SBH, Botti P;
WPI; 2000-270792/23.
Selectively labeled membrane peptides, useful e.g. for detecting ligand binding to receptors and in drug screening, are prepared, in lipid matrix, by reaction between amino acid residues
Example 11; Page 68-69; 120pp; English.
New methods are described by which membrane polypeptides can be labelled. The method comprises chemoselective chemical ligation of the membrane polypeptide which is incorporated in a lipid matrix, and a ligation label. Both contain an amino acid having an unprotected reactive group that together undergo chemoselective ligation to form a covalent bond. The method can be used to label folded polypeptides embedded in a lipid membrane, by treating the polypeptide with a reagent that cleaves specifically adjacent to an amino acid with an unprotected reactive group and then ligating the cleaved polypeptide with the ligation label. The ligation label can be a chromophore, thus ligand binding to membrane bound polypeptides can be detected by contacting a membrane bound polypeptide comprising a chromophore, with the ligand under investigation and screening for binding in an assay characterized by detecting fluorescence resonance energy transfer (FRET) between the chromophore and a second chromophore, the chromophores comprising a donor and acceptor pair of a resonance energy transfer system. The methods are used for lipid matrix-assisted chemical ligation and synthesis of membrane polypeptides. Labeled membrane polypeptides are used to detect ligand binding and the identification of receptor domains, e.g. for structure/activity studies. They can also be used in drug screening, selection or design, and for diagnosis. The methods are particularly used for fluorescent resonance energy transfer (FRET) analysis of site-specific incorporation of labels during polypeptide synthesis and analysis of previously inaccessible membrane proteins. This sequence is the sequence of Melanocortin receptor MC4 which also comprises a Factor Xa cleavage site. Cleavage with Factor Xa gives a C-terminal alpha-thioester modified MC4 receptor ligation label (AA83183) and an MC4 receptor membrane polypeptide cleavage product (AA83184). Chemical ligation of cleaved MC4 in alternative membrane patches or micelles to an MC4 ligation label produces the synthetic labeled MC4 product (AA83185).

AA83185 standard; peptide; 332 AA.
AA83185;
24-JUL-2000 (first entry)
Synthetic labeled melanocortin receptor MC4.
Membrane polypeptide; lipid matrix; synthesis; ligation; chemoselective ligation; fluorescence resonance energy transfer; FRET; chromophore; ligand; receptor domain; drug screening; diagnosis; ion channel; melanocortin receptor; MC4.
Synthetic.
Homo sapiens.
WO200012536-A2.
09-MAR-2000.
26-AUG-1999; 99WO-US19542.
31-AUG-1998; 98US-0144964.
05-MAR-1999; 99US-0263971.
(GRYP-) GRYPHON SCI.
Kochendoerfer GG, Hunter CL, Kent SBH, Botti P;
WPI; 2000-270792/23.
Selectively labeled membrane peptides, useful e.g. for detecting ligand binding to receptors and in drug screening, are prepared, in lipid matrix, by reaction between amino acid residues
Example 11; Page 71; 120pp; English.
New methods are described by which membrane polypeptides can be labelled. The method comprises chemoselective chemical ligation of the membrane polypeptide which is incorporated in a lipid matrix, and a ligation label. Both contain an amino acid having an unprotected reactive group that together undergo chemoselective ligation to form a covalent bond. The method can be used to label folded polypeptides embedded in a lipid membrane, by treating the polypeptide with a reagent that cleaves specifically adjacent to an amino acid with an unprotected reactive group and then ligating the cleaved polypeptide with the ligation label. The ligation label can be a chromophore, thus ligand binding to membrane bound polypeptides can be detected by contacting a membrane bound polypeptide comprising a chromophore, with the ligand under investigation and screening for binding in an assay characterized by detecting fluorescence resonance energy transfer (FRET) between the chromophore and a second chromophore, the chromophores comprising a donor and acceptor pair of a resonance energy transfer system. The methods are used for lipid matrix-assisted chemical ligation and synthesis of membrane polypeptides. Labeled membrane polypeptides are used to detect ligand binding and the identification of receptor domains, e.g. for structure/activity studies. They can also be used in drug screening, selection or design, and for diagnosis. The methods are particularly used for fluorescent resonance energy transfer (FRET) analysis of site-specific incorporation of labels during polypeptide synthesis and analysis of previously inaccessible membrane proteins. A C-terminal alpha-thioester modified MC4 receptor ligation label (AA83183) and an MC4 receptor membrane polypeptide cleavage product (AA83184). Chemical ligation of cleaved MC4 in alternative membrane patches or micelles to an MC4 ligation label produces the synthetic labeled MC4 product (AA83185).

RESULT 37
AA83185

Query Match 5.0%; Score 7; DB 21; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

Sequence 332 AA;

Query Match 5.0%; Score 7; DB 21; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

52 VLPGTGA 58
228 VLPGTGA 234

RESULT 38
AY87415
ID AAY87415 standard; protein; 332 AA.

AY87415;
03-JUL-2000 (first entry)
Melanocortin-4 receptor (MC4-R).
Melanocortin-4 receptor; MC4-R; inhibitor; addictive behaviour;
drug addiction; cocaine; morphine; obsessive-compulsive disorder.

Mammalia.
WO200014115-A1.
16-MAR-2000.
30-AUG-1999; 99WO-US19790.
03-SEP-1998; 98US-0099104.
(MILL-) MILLENNIUM PHARM INC.
Duman R;

WPI; 2000-256944/22.

Identification of compounds that regulate addictive behavior for
treatment of addictive behavior disorders, such as obsessive-compulsive
disease, comprises determining whether compounds are antagonists to
melanocortin-4 receptor -

Claim 1; Fig 1; 62pp; English.

The invention relates to methods for the identification of compounds
that regulate addictive behaviour, particularly drug addiction. The
method comprises determining whether a test compound can bind to and
antagonise a melanocortin-4 receptor (MC4-R), and administering that
compound to an animal in order to see if a reduction in addictive
behaviour occurs. Melanocortins are products of pro-opiomelanocortin
post-translational processing which are thought to have a broad range of
physiological actions, including behaviour, learning, memory, analgesia,
thermoregulation and body weight, as well as their well known effects on
adrenal cortical functions and on melanocytes. The present invention is
based on the observations that MC4-R activity potentiates some of the
addictive effects of drugs of addiction, particularly cocaine and
morphine, and that knockout mice do not display the behavioural responses
indicative of addiction caused by chronic and/or acute administration of
these drugs. The methods are useful for identifying MC4-R inhibitors.
These compounds may be used to treat addiction to a wide variety of
substances, including cocaine, opiates, alcohol, hallucinogens, minor
tranquillisers, nicotine and stimulants. The methods are also useful for
the treatment of addictive behaviour disorders, including extreme
craving, addictive psychological disease or obsessive-compulsive
disorder. The present sequence represents a mammalian MC4-R.

Sequence 332 AA;

Query Match 5.0%; Score 7; DB 21; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
DB 228 VLPGTGA 234

RESULT 39
AAB68490
ID AAB68490 standard; Protein; 332 AA.

AAB68490;
23-JUL-2001 (first entry)
Amino acid sequence of a human melanocortin-4 receptor (MC-R4).
Human; melanocortin-4 receptor; MC-R4; transgenic animal; body weight;
food intake; obesity; diabetes; anorexia; cachexia; cancer;
sexual dysfunction; pain; impaired memory; neuronal regeneration;
neuropathy; growth disorder; growth hormone;
insulin-like growth factor-1.

Homo sapiens.
WO200133956-A1.
17-MAY-2001.
13-NOV-2000; 2000WO-US31061.
12-NOV-1999; 99US-0165074.
(MERI) MERCK & CO INC.

Van Der Ploeg LHT, Chen AS, Chen HY, Forrest MJ, MacIntyre DB;
Metzger JM, Palyha OC, Feighner SD, Hreniuk D;

WPI; 2001-343541/36.
N-PSDB; AAF85465.

New transgenic animal with non-functional gene for melanocortin-4
receptor, useful for identifying specific modulators, potentially used
for treating obesity or diabetes -

Disclosure; Fig 2; 58pp; English.

The present sequence represents a human melanocortin-4 receptor (MC-R4).
The specification describes transgenic non-human animals whose somatic
cells contain at least one non-functional gene for MC-R4
protein. The transgenic animals, or cells derived from them, are used
to screen for compounds that modulate MC-R4. These modulators are
potentially useful for regulating body weight and food intake and
treatment of associated diseases, obesity; diabetes; anorexia; cachexia;
cancer; sexual dysfunction; pain; impaired memory or neuronal
regeneration; neuropathy; growth disorders linked to growth hormone
and insulin-like growth factor-1. They can also be used to study MC-R4
expression and activity.

Sequence 332 AA;
Query Match 5.0%; Score 7; DB 22; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
DB 228 VLPGTGA 234

RESULT 40
AAE15746
ID AAE15746 standard; Protein; 332 AA.

AAE15746;

Search completed: November 14, 2003, 10:50:35
Job time : 55 secs

XX 26-MAR-2002 (first entry)
DT Human melanocortin 4-receptor (MC4R).
XX
XX
XX Human; single nucleotide polymorphism; SNP; melanocortin 4-receptor;
KW MC4R; haplotype; obesity; screening; allele-specific oligonucleotide;
KW ASO; gene therapy; anorectic; chromosome 18q22.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Misc-difference 103
FT /note= "Ile at this position is replaced with Val
FT due to single nucleotide polymorphism"
FT
FT Misc-difference 176
FT /note= "Ala at this position is replaced with Val
FT due to single nucleotide polymorphism"
FT
FT Misc-difference 202
FT /note= "Phe at this position is replaced with Leu
FT due to single nucleotide polymorphism"
FT
FT Misc-difference 251
FT /note= "Ile at this position is replaced with Leu
FT due to single nucleotide polymorphism"
XX
XX WO200179222-A2.
PN
XX
XX 25-OCT-2001.
PD
XX
XX 12-APR-2001; 2001WO-US11943.
PF
XX
XX 12-APR-2000; 2000US-196677P.
PR
XX
XX (GENA-) GENAISANCE PHARM INC.
PA
XX Bentivegna SC, Choi JY, Kazemi A, Lee HH, Nandabalan K, Parks KE;
PI Sausker EA;
PI
XX WPI; 2002-082744/11.
DR N-PSDB; AAD25896, AAD25897.
XX
XX Novel polymorphic variants of melanocortin 4-receptor gene useful in
PT studying expression and function of the protein, useful for screening
PT candidate drugs to treat diseases related to the protein activity e.g.
PT obesity -
XX
XX Claim 27; Fig 3; 53pp; English.
PS
XX The invention relates to single nucleotide polymorphisms (SNP) in human
XX melanocortin 4-receptor (MC4R) gene. MC4R gene haplotypes are useful
XX for improving the efficiency and reliability of several steps in the
XX discovery and development of drugs for treating diseases associated
XX with MC4R activity, e.g. obesity. MC4R gene is useful in studying the
XX expression and function of MC4R and in expressing MC4R protein for
XX use in screening for candidate drugs to treat diseases related to
XX MC4R activity and in studying the effect of the variation on the
XX biological activity of MC4R as well as on the binding affinity of
XX candidate drugs targeting MC4R for the treatment of obesity. MC4R
XX antibody is useful in a variety of diagnostic and prognostic formats
XX and in therapeutic methods. Allele-specific oligonucleotide (ASO) is
XX useful as probes and primers, and for assaying a polymorphism in
XX MC4R gene. MC4R DNA is used in gene therapy. The present sequence is
XX human MC4R protein. MC4R gene is located on chromosome 18q22.
XX
XX Sequence 332 AA;
SQ

Query Match 5.0%; Score 7; DB 23; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 52 VLPGTGA 58
Db 228 VLPGTGA 234

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OM protein - protein search, using sw model

Run on: November 14, 2003, 10:49:31 ; Search time 43 Seconds
(without alignments)
138,740 Million cell updates/sec

Title: US-10-087-573-2
Perfect score: 141
Sequence: 1 MESTSTTNFVAENRPTFGE.....RAEYFRLHLSLKSGVNRLLI 141

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/aaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/aaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/aaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/aaa/PTUS-COMB.pep.*
6: /cgn2_6/ptodata/1/aaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	5.0	32	4	US-09-230-041-42
2	7	5.0	35	4	US-09-230-041-37
3	7	5.0	291	4	US-09-384-302A-8
4	7	5.0	320	4	US-09-325-932A-190
5	7	5.0	332	1	US-08-671-525B-8
6	7	5.0	332	1	US-08-672-109B-8
7	7	5.0	332	2	US-08-842-045-8
8	7	5.0	332	2	US-08-842-238-8
9	7	5.0	332	2	US-08-652-560-2
10	7	5.0	332	2	US-08-780-749A-2
11	7	5.0	332	2	US-08-780-749A-6
12	7	5.0	332	3	US-08-706-281A-16
13	7	5.0	332	3	US-08-629-335B-8
14	7	5.0	332	3	US-09-097-231-16
15	7	5.0	332	3	US-08-870-511-2
16	7	5.0	332	3	US-08-870-511-6
17	7	5.0	332	3	US-08-870-511-8
18	7	5.0	332	3	US-08-870-511-10
19	7	5.0	332	3	US-08-870-511-12
20	7	5.0	332	4	US-09-384-302A-6
21	7	5.0	332	4	US-09-384-302A-9
22	7	5.0	332	4	US-09-353-099-16
23	7	5.0	332	4	US-09-831-206-2
24	7	5.0	341	4	US-09-252-991A-29610
25	7	5.0	354	4	US-09-252-991A-31144
26	7	5.0	516	4	US-09-328-352-647A
27	7	5.0	522	4	US-09-328-352-6840

28	7	5.0	525	4	US-09-328-352-6683	Sequence 6683, Ap
29	7	5.0	538	4	US-09-252-991A-23068	Sequence 23068, A
30	6	4.3	15	1	US-08-268-251-19	Sequence 19, Appl
31	6	4.3	15	5	PCT-US93-01112-19	Sequence 19, Appl
32	6	4.3	20	4	US-09-205-258-1217	Sequence 1217, Ap
33	6	4.3	23	1	US-08-268-251-49	Sequence 49, Appl
34	6	4.3	23	5	PCT-US93-01112-49	Sequence 38, Appl
35	6	4.3	34	1	US-08-658-136-38	Sequence 8, Appl
36	6	4.3	41	1	US-08-179-632-8	Sequence 8, Appl
37	6	4.3	41	1	US-08-440-174B-8	Sequence 8, Appl
38	6	4.3	41	5	PCT-US95-00062-8	Sequence 8, Appl
39	6	4.3	55	4	US-09-205-258-1215	Sequence 1215, Ap
40	6	4.3	63	4	US-09-134-001C-2886	Sequence 2886, Ap
41	6	4.3	74	4	US-09-732-210-387	Sequence 387, Ap
42	6	4.3	76	1	US-08-519-777-22	Sequence 22, Appl
43	6	4.3	76	1	US-08-742-035-22	Sequence 22, Appl
44	6	4.3	76	2	US-08-777-019-22	Sequence 22, Appl
45	6	4.3	76	2	US-08-777-143-22	Sequence 22, Appl
46	6	4.3	76	3	US-08-775-414-22	Sequence 22, Appl
47	6	4.3	76	3	US-08-931-858B-22	Sequence 22, Appl
48	6	4.3	76	3	US-08-981-739-22	Sequence 22, Appl
49	6	4.3	76	4	US-09-128-026-22	Sequence 22, Appl
50	6	4.3	77	2	US-08-102-385G-29	Sequence 29, Appl
51	6	4.3	88	4	US-09-300-008B-59	Sequence 59, Appl
52	6	4.3	93	4	US-09-450-072-75	Sequence 75, Appl
53	6	4.3	93	4	US-09-351-348-75	Sequence 75, Appl
54	6	4.3	95	1	US-08-519-777-24	Sequence 24, Appl
55	6	4.3	95	1	US-08-742-035-24	Sequence 24, Appl
56	6	4.3	95	2	US-08-777-019-24	Sequence 24, Appl
57	6	4.3	95	2	US-08-777-143-24	Sequence 24, Appl
58	6	4.3	95	3	US-08-775-414-24	Sequence 24, Appl
59	6	4.3	95	3	US-08-931-858B-24	Sequence 24, Appl
60	6	4.3	95	3	US-08-981-739-24	Sequence 24, Appl
61	6	4.3	95	4	US-09-128-026-24	Sequence 24, Appl
62	6	4.3	108	4	US-09-252-991A-28388	Sequence 28388, A
63	6	4.3	111	1	US-08-543-238-8	Sequence 8, Appl
64	6	4.3	111	1	US-08-420-526-8	Sequence 8, Appl
65	6	4.3	131	1	US-07-893-929A-1	Sequence 1, Appl
66	6	4.3	131	5	PCT-US92-10344-1	Sequence 1, Appl
67	6	4.3	133	4	US-09-252-991A-19617	Sequence 19617, A
68	6	4.3	138	4	US-09-252-991A-19261	Sequence 19261, A
69	6	4.3	138	4	US-09-252-991A-28372	Sequence 28372, A
70	6	4.3	142	3	US-08-775-414-82	Sequence 82, Appl
71	6	4.3	145	4	US-09-252-991A-28923	Sequence 28923, A
72	6	4.3	150	3	US-08-775-414-84	Sequence 84, Appl
73	6	4.3	156	4	US-09-252-991A-17905	Sequence 17905, A
74	6	4.3	163	4	US-09-134-001C-3109	Sequence 3109, Ap
75	6	4.3	165	4	US-09-252-991A-17601	Sequence 17601, A
76	6	4.3	176	3	US-09-309-317-2	Sequence 2, Appl
77	6	4.3	176	4	US-09-252-991A-24888	Sequence 24888, A
78	6	4.3	176	4	US-09-732-210-1080	Sequence 1080, Ap
79	6	4.3	177	5	PCT-US96-03916-19	Sequence 19, Appl
80	6	4.3	179	3	US-09-309-317-3	Sequence 3, Appl
81	6	4.3	179	3	US-09-309-317-4	Sequence 4, Appl
82	6	4.3	192	4	US-09-134-001C-4329	Sequence 4329, Ap
83	6	4.3	195	1	US-08-519-777-8	Sequence 8, Appl
84	6	4.3	195	2	US-08-742-035-8	Sequence 8, Appl
85	6	4.3	195	2	US-08-777-019-8	Sequence 8, Appl
86	6	4.3	195	2	US-08-777-143-8	Sequence 8, Appl
87	6	4.3	195	3	US-08-775-414-8	Sequence 8, Appl
88	6	4.3	195	3	US-08-931-858B-8	Sequence 8, Appl
89	6	4.3	195	3	US-08-981-739-8	Sequence 8, Appl
90	6	4.3	195	4	US-09-128-036-8	Sequence 8, Appl
91	6	4.3	196	5	PCT-US91-09055-6	Sequence 6, Appl
92	6	4.3	197	4	US-09-252-991A-16918	Sequence 16918, A
93	6	4.3	200	2	US-08-682-517-20	Sequence 20, Appl
94	6	4.3	203	4	US-09-252-991A-32730	Sequence 32730, A
95	6	4.3	205	2	US-08-852-809-5	Sequence 5, Appl
96	6	4.3	206	4	US-09-198-452A-273	Sequence 273, Ap
97	6	4.3	217	4	US-09-252-991A-19413	Sequence 19413, A
98	6	4.3	217	4	US-09-198-452A-656	Sequence 656, Ap
99	6	4.3	219	4	US-09-252-991A-18278	Sequence 18278, A
100	6	4.3	226	4	US-09-198-452A-210	Sequence 210, Ap

101	6	4.3	235	4	US-09-252-991A-18051	Sequence 18051, A	174	6	4.3	400	3	US-09-213-053-5	Sequence 5, Appli
102	6	4.3	236	4	US-09-252-991A-27618	Sequence 27618, A	175	6	4.3	400	3	US-08-450-962-4	Sequence 4, Appli
103	6	4.3	237	4	US-09-134-001C-4213	Sequence 4213, Ap	176	6	4.3	400	3	US-08-450-962-6	Sequence 6, Appli
104	6	4.3	238	4	US-09-071-035-156	Sequence 156, App	177	6	4.3	401	3	US-08-289-222B-3	Sequence 3, Appli
105	6	4.3	245	4	US-09-252-991A-19505	Sequence 19505, A	178	6	4.3	401	3	US-09-054-526B-3	Sequence 3, Appli
106	6	4.3	246	4	US-09-252-991A-20016	Sequence 20016, A	179	6	4.3	403	2	US-09-061-337-10	Sequence 10, Appl
107	6	4.3	248	4	US-09-328-352-6994	Sequence 6994, Ap	180	6	4.3	403	2	US-09-122-129-10	Sequence 10, Appl
108	6	4.3	253	4	US-09-252-991A-19036	Sequence 19036, A	181	6	4.3	403	3	US-09-340-991-10	Sequence 10, Appl
109	6	4.3	257	4	US-09-252-991A-31359	Sequence 31359, A	182	6	4.3	403	3	US-08-374-609-10	Sequence 10, Appl
110	6	4.3	261	4	US-09-134-001C-4935	Sequence 4935, Ap	183	6	4.3	403	4	US-09-549-098-10	Sequence 10, Appl
111	6	4.3	262	4	US-09-107-532A-4837	Sequence 4837, Ap	184	6	4.3	403	4	US-09-252-991A-23081	Sequence 23081, A
112	6	4.3	263	4	US-09-107-532A-4837	Sequence 4837, Ap	185	6	4.3	404	4	US-09-252-991A-17418	Sequence 17418, A
113	6	4.3	264	4	US-09-996-243-28	Sequence 28, Appl	186	6	4.3	410	1	US-08-471-033-40	Sequence 40, Appl
114	6	4.3	267	4	US-09-071-035-154	Sequence 154, App	187	6	4.3	410	1	US-08-471-033-43	Sequence 43, Appl
115	6	4.3	273	4	US-09-252-991A-28324	Sequence 28324, A	188	6	4.3	410	2	US-08-471-044-40	Sequence 40, Appl
116	6	4.3	274	3	US-08-482-918-51	Sequence 51, Appl	189	6	4.3	410	2	US-08-471-044-43	Sequence 43, Appl
117	6	4.3	274	3	US-09-224-681-51	Sequence 51, Appl	190	6	4.3	410	2	US-08-463-483A-40	Sequence 40, Appl
118	6	4.3	274	3	US-08-336-728A-51	Sequence 51, Appl	191	6	4.3	410	2	US-08-463-483A-43	Sequence 43, Appl
119	6	4.3	278	4	US-09-328-352-5824	Sequence 5824, Ap	192	6	4.3	410	2	US-08-471-046A-40	Sequence 40, Appl
120	6	4.3	279	4	US-09-107-532A-6998	Sequence 6998, Ap	193	6	4.3	410	2	US-08-471-046A-43	Sequence 43, Appl
121	6	4.3	287	4	US-08-311-731A-232	Sequence 232, App	194	6	4.3	410	2	US-08-470-566B-40	Sequence 40, Appl
122	6	4.3	288	4	US-09-216-393B-341	Sequence 341, App	195	6	4.3	410	2	US-08-470-566B-43	Sequence 43, Appl
123	6	4.3	288	4	US-09-216-393B-341	Sequence 341, App	196	6	4.3	410	2	US-08-469-334-40	Sequence 40, Appl
124	6	4.3	294	1	US-08-433-783-38	Sequence 38, Appl	197	6	4.3	410	2	US-08-469-334-43	Sequence 43, Appl
125	6	4.3	294	2	US-08-337-358-38	Sequence 38, Appl	198	6	4.3	410	3	US-09-300-529-40	Sequence 40, Appl
126	6	4.3	294	5	PCT-US95-07537A-38	Sequence 38, Appl	199	6	4.3	410	3	US-09-300-529-43	Sequence 43, Appl
127	6	4.3	294	5	PCT-US95-07537A-38	Sequence 38, Appl	200	6	4.3	420	4	US-09-252-991A-16912	Sequence 16912, A
128	6	4.3	299	4	US-09-328-352-4146	Sequence 4146, Ap	201	6	4.3	422	4	US-09-679-279-17	Sequence 17, Appl
129	6	4.3	300	4	US-09-328-352-4146	Sequence 4146, Ap	202	6	4.3	423	4	US-09-107-532A-6847	Sequence 6847, Ap
130	6	4.3	305	4	US-09-252-991A-22845	Sequence 22845, A	203	6	4.3	425	4	US-08-450-962-4	Sequence 25840, A
131	6	4.3	307	3	US-09-049-672A-9	Sequence 9, Appli	204	6	4.3	428	4	US-09-252-991A-23349	Sequence 23349, A
132	6	4.3	315	4	US-09-252-991A-26703	Sequence 26703, A	205	6	4.3	428	4	US-08-657-641-6	Sequence 6, Appli
133	6	4.3	319	1	US-08-597-485B-22	Sequence 22, Appl	206	6	4.3	428	5	PCT-US94-07233-6	Sequence 6, Appli
134	6	4.3	319	3	US-09-068-051A-22	Sequence 22, Appl	207	6	4.3	446	1	US-07-626-618A-21	Sequence 21, Appl
135	6	4.3	319	4	US-09-336-536-67	Sequence 67, Appl	208	6	4.3	446	1	US-07-626-618A-22	Sequence 22, Appl
136	6	4.3	319	4	US-09-254-465A-6	Sequence 6, Appli	209	6	4.3	446	1	US-08-333-977-21	Sequence 21, Appl
137	6	4.3	326	1	US-08-053-867A-2	Sequence 2, Appli	210	6	4.3	446	1	US-08-333-977-22	Sequence 22, Appl
138	6	4.3	326	1	US-08-053-867A-2	Sequence 2, Appli	211	6	4.3	446	2	US-07-369-267B-4	Sequence 4, Appli
139	6	4.3	327	3	US-08-560-780-23	Sequence 23, Appl	212	6	4.3	446	3	US-08-560-780-52	Sequence 52, Appl
140	6	4.3	327	3	US-08-960-780-29	Sequence 29, Appl	213	6	4.3	446	3	US-09-073-898-52	Sequence 52, Appl
141	6	4.3	327	3	US-09-073-898-23	Sequence 23, Appl	214	6	4.3	446	4	US-09-168-510-4	Sequence 4, Appli
142	6	4.3	327	3	US-09-073-898-29	Sequence 29, Appl	215	6	4.3	449	1	US-08-471-033-46	Sequence 46, Appl
143	6	4.3	331	2	US-08-245-511-58	Sequence 58, Appl	216	6	4.3	449	1	US-08-471-044-46	Sequence 46, Appl
144	6	4.3	331	2	US-08-600-993A-58	Sequence 58, Appl	217	6	4.3	449	2	US-08-463-483A-46	Sequence 46, Appl
145	6	4.3	338	1	US-08-218-686-2	Sequence 2, Appli	218	6	4.3	449	2	US-08-471-046A-46	Sequence 46, Appl
146	6	4.3	338	3	US-08-460-242-2	Sequence 2, Appli	219	6	4.3	449	2	US-08-470-566B-46	Sequence 46, Appl
147	6	4.3	339	4	US-09-198-452A-1067	Sequence 1067, Ap	220	6	4.3	449	3	US-09-300-529-46	Sequence 46, Appl
148	6	4.3	342	2	US-08-899-011-2	Sequence 2, Appli	221	6	4.3	449	3	US-08-469-334-46	Sequence 46, Appl
149	6	4.3	342	3	US-09-373-958-2	Sequence 2, Appli	222	6	4.3	450	4	US-09-300-529-46	Sequence 26266, A
150	6	4.3	343	2	US-08-446-875-2	Sequence 2, Appli	223	6	4.3	450	6	5194375-6	Patent No. 5194375
151	6	4.3	343	2	US-08-102-385G-2	Sequence 2, Appli	224	6	4.3	452	1	US-08-471-033-2	Sequence 2, Appli
152	6	4.3	345	4	US-09-252-991A-23059	Sequence 23059, A	225	6	4.3	462	1	US-08-471-033-20	Sequence 20, Appl
153	6	4.3	357	4	US-09-198-452A-487	Sequence 487, App	226	6	4.3	462	2	US-08-471-044-2	Sequence 2, Appli
154	6	4.3	364	4	US-09-417-485D-41	Sequence 41, Appl	227	6	4.3	462	2	US-08-471-044-20	Sequence 20, Appl
155	6	4.3	372	4	US-09-556-870A-2	Sequence 2, Appli	228	6	4.3	462	2	US-08-463-483A-2	Sequence 2, Appli
156	6	4.3	373	1	US-08-118-270-24	Sequence 24, Appl	229	6	4.3	462	2	US-08-463-483A-20	Sequence 20, Appl
157	6	4.3	373	5	PCT-US93-08528-24	Sequence 24, Appl	230	6	4.3	462	2	US-08-471-046A-2	Sequence 2, Appli
158	6	4.3	383	1	US-08-597-545-2	Sequence 2, Appli	231	6	4.3	462	2	US-08-471-046A-20	Sequence 20, Appl
159	6	4.3	383	1	US-08-457-135-2	Sequence 2, Appli	232	6	4.3	462	2	US-08-470-566B-2	Sequence 2, Appli
160	6	4.3	388	1	US-08-087-772A-2	Sequence 2, Appli	233	6	4.3	462	2	US-08-470-566B-20	Sequence 20, Appl
161	6	4.3	388	2	US-08-894-772-2	Sequence 2, Appli	234	6	4.3	462	2	US-08-469-334-2	Sequence 2, Appli
162	6	4.3	388	2	US-09-207-844-2	Sequence 2, Appli	235	6	4.3	462	2	US-08-469-334-20	Sequence 20, Appl
163	6	4.3	396	2	US-09-122-129-12	Sequence 12, Appl	236	6	4.3	462	3	US-09-300-529-2	Sequence 2, Appli
164	6	4.3	396	2	US-09-122-129-12	Sequence 12, Appl	237	6	4.3	462	3	US-09-300-529-20	Sequence 20, Appl
165	6	4.3	396	3	US-08-974-609-12	Sequence 12, Appl	238	6	4.3	465	4	US-09-328-352-6141	Sequence 6141, Ap
166	6	4.3	396	3	US-09-461-474-2	Sequence 2, Appli	239	6	4.3	471	4	US-09-252-991A-4629	Sequence 4629, Ap
167	6	4.3	396	3	US-09-242-859A-6	Sequence 6, Appli	240	6	4.3	476	4	US-09-107-532A-4629	Sequence 23248, A
168	6	4.3	396	4	US-09-242-859A-6	Sequence 6, Appli	241	6	4.3	479	4	US-09-134-001C-3778	Sequence 3778, Ap
169	6	4.3	396	4	US-09-549-098-12	Sequence 12, Appl	242	6	4.3	481	5	US-09-996-243-216	Sequence 216, App
170	6	4.3	397	4	US-09-252-991A-20592	Sequence 20592, A	243	6	4.3	483	4	PCT-US91-02166-13	Sequence 13, Appl
171	6	4.3	399	4	US-09-252-991A-32906	Sequence 32906, A	244	6	4.3	483	4	US-09-904-615-154	Sequence 154, App
172	6	4.3	400	1	US-08-351-473B-5	Sequence 5, Appli	245	6	4.3	487	1	US-08-444-734A-2	Sequence 2, Appli
173	6	4.3					246	6	4.3	488	2	US-08-695-412B-10	Sequence 10, Appl

247	6	4.3	488	4	US-09-255-154D-10	Sequence 10, Appl	320	6	4.3	873	1	US-08-909-983-6	Sequence 6, Appl
248	6	4.3	490	4	US-09-461-325-250	Sequence 250, App	321	6	4.3	875	1	US-08-571-758-8	Sequence 8, Appl
249	6	4.3	490	4	US-09-461-325-518	Sequence 518, App	322	6	4.3	875	1	US-08-909-984A-8	Sequence 8, Appl
250	6	4.3	491	1	US-08-206-176-4	Sequence 4, Appl	323	6	4.3	875	1	US-08-909-983-8	Sequence 8, Appl
251	6	4.3	492	4	US-09-794-236-2	Sequence 2, Appl	324	6	4.3	875	3	US-09-150-460B-7	Sequence 7, Appl
252	6	4.3	492	4	US-09-345-469-1	Sequence 1, Appl	325	6	4.3	884	2	US-09-585-858-18	Sequence 18, Appl
253	6	4.3	495	1	US-08-455-559-10	Sequence 10, Appl	326	6	4.3	884	2	US-08-465-976A-2	Sequence 2, Appl
254	6	4.3	495	3	US-09-145-060-10	Sequence 10, Appl	327	6	4.3	884	2	US-08-982-412-2	Sequence 2, Appl
255	6	4.3	495	4	US-09-252-991A-26109	Sequence 26109, A	328	6	4.3	915	3	US-08-472-240A-8	Sequence 8, Appl
256	6	4.3	495	5	PCT-US94-06657-10	Sequence 10, Appl	329	6	4.3	923	3	US-09-252-991A-22409	Sequence 22409, A
257	6	4.3	497	4	US-09-252-991A-22660	Sequence 22660, A	330	6	4.3	928	3	US-09-320-878-13	Sequence 13, Appl
258	6	4.3	501	2	US-08-288-508C-2	Sequence 2, Appl	331	6	4.3	928	3	US-09-105-537-41	Sequence 41, Appl
259	6	4.3	501	4	US-08-981-490B-1	Sequence 1, Appl	332	6	4.3	928	3	US-09-141-508-14	Sequence 14, Appl
260	6	4.3	506	4	US-09-252-991A-27436	Sequence 27436, A	333	6	4.3	928	4	US-09-657-440-13	Sequence 13, Appl
261	6	4.3	509	2	US-09-031-392-6	Sequence 6, Appl	334	6	4.3	929	4	US-09-252-991A-22946	Sequence 22946, A
262	6	4.3	509	3	US-09-299-549-6	Sequence 6, Appl	335	6	4.3	934	4	US-09-252-991A-25635	Sequence 25635, A
263	6	4.3	509	4	US-09-610-417-6	Sequence 6, Appl	336	6	4.3	1064	1	US-08-537-210A-3	Sequence 3, Appl
264	6	4.3	515	4	US-09-461-325-219	Sequence 219, App	337	6	4.3	1064	3	US-09-113-825-3	Sequence 3, Appl
265	6	4.3	527	4	US-08-823-516-144	Sequence 144, App	338	6	4.3	1067	4	US-09-252-991A-30526	Sequence 30526, A
266	6	4.3	537	4	US-09-388-413B-6	Sequence 6, Appl	339	6	4.3	1078	4	US-08-264-534-32	Sequence 32, Appl
267	6	4.3	540	4	US-09-328-352-4514	Sequence 4514, Ap	340	6	4.3	1078	1	US-08-083-590A-11	Sequence 11, Appl
268	6	4.3	550	2	US-08-823-516-142	Sequence 142, App	341	6	4.3	1078	1	US-08-465-500-32	Sequence 32, Appl
269	6	4.3	550	4	US-09-198-452A-613	Sequence 613, App	342	6	4.3	1078	2	US-08-346-128-32	Sequence 32, Appl
270	6	4.3	553	4	US-09-252-991A-17429	Sequence 17429, A	343	6	4.3	1078	3	US-08-532-384-11	Sequence 11, Appl
271	6	4.3	558	4	US-09-328-352-4870	Sequence 4870, Ap	344	6	4.3	1078	3	US-08-893-828-32	Sequence 32, Appl
272	6	4.3	567	2	US-08-504-459-2	Sequence 2, Appl	345	6	4.3	1081	4	US-09-394-272-4	Sequence 4, Appl
273	6	4.3	570	4	US-09-252-991A-26331	Sequence 26331, A	346	6	4.3	1088	2	US-08-742-026-2	Sequence 2, Appl
274	6	4.3	574	4	US-09-134-001C-5409	Sequence 5409, Ap	347	6	4.3	1088	2	US-08-742-026-23	Sequence 23, Appl
275	6	4.3	578	4	US-09-328-352-5679	Sequence 5679, Ap	348	6	4.3	1128	4	US-09-252-991A-19672	Sequence 19672, A
276	6	4.3	594	4	US-09-252-991A-28139	Sequence 28139, A	349	6	4.3	1220	2	US-08-680-326-38	Sequence 38, Appl
277	6	4.3	602	4	US-09-374-454-19	Sequence 19, Appl	350	6	4.3	1223	4	US-09-071-035-236	Sequence 236, App
278	6	4.3	607	4	US-09-252-991A-32643	Sequence 32643, A	351	6	4.3	1223	1	US-08-026-138B-3	Sequence 3, Appl
279	6	4.3	623	4	US-09-252-991A-21205	Sequence 21205, A	352	6	4.3	1253	3	US-08-252-966B-12	Sequence 12, Appl
280	6	4.3	623	4	US-09-071-035-244	Sequence 244, App	353	6	4.3	1253	3	US-08-947-823-3	Sequence 3, Appl
281	6	4.3	631	4	US-09-252-991A-26444	Sequence 26444, A	354	6	4.3	1261	3	US-08-252-966B-18	Sequence 18, Appl
282	6	4.3	631	4	US-09-107-532A-6577	Sequence 6577, Ap	355	6	4.3	1290	3	US-09-150-460B-6	Sequence 6, Appl
283	6	4.3	632	1	US-08-443-104-4	Sequence 4, Appl	356	6	4.3	1301	4	US-09-071-035-234	Sequence 234, App
284	6	4.3	632	1	US-08-442-859-4	Sequence 4, Appl	357	6	4.3	1301	4	US-09-071-035-238	Sequence 238, App
285	6	4.3	632	2	US-08-398-489-4	Sequence 4, Appl	358	6	4.3	1301	4	US-09-071-035-242	Sequence 242, App
286	6	4.3	632	5	PCT-US95-05534-4	Sequence 4, Appl	359	6	4.3	1301	4	US-09-252-991A-29822	Sequence 29822, A
287	6	4.3	635	1	US-08-571-758-10	Sequence 10, Appl	360	6	4.3	1338	1	US-08-471-033-50	Sequence 50, Appl
288	6	4.3	635	1	US-08-909-984A-10	Sequence 10, Appl	361	6	4.3	1338	2	US-08-471-044-50	Sequence 50, Appl
289	6	4.3	635	1	US-08-909-983-10	Sequence 10, Appl	362	6	4.3	1338	2	US-08-463-483A-50	Sequence 50, Appl
290	6	4.3	645	2	US-08-785-430-2	Sequence 2, Appl	363	6	4.3	1338	2	US-08-471-046A-50	Sequence 50, Appl
291	6	4.3	645	2	US-08-996-800-2	Sequence 2, Appl	364	6	4.3	1338	2	US-08-470-566B-50	Sequence 50, Appl
292	6	4.3	650	4	US-09-134-001C-1781	Sequence 3781, Ap	365	6	4.3	1338	2	US-08-469-334-50	Sequence 50, Appl
293	6	4.3	675	4	US-09-252-991A-27987	Sequence 27987, A	366	6	4.3	1338	3	US-09-300-529-50	Sequence 50, Appl
294	6	4.3	683	4	US-09-252-991A-28674	Sequence 28674, A	367	6	4.3	1346	1	US-08-471-033-23	Sequence 23, Appl
295	6	4.3	698	4	US-09-107-532A-5685	Sequence 5685, Ap	368	6	4.3	1346	2	US-08-471-044-23	Sequence 23, Appl
296	6	4.3	704	1	US-08-188-582-18	Sequence 18, Appl	369	6	4.3	1346	2	US-08-463-483A-23	Sequence 23, Appl
297	6	4.3	704	1	US-08-646-715-18	Sequence 18, Appl	370	6	4.3	1346	2	US-08-471-046A-23	Sequence 23, Appl
298	6	4.3	705	4	US-09-370-838-186	Sequence 186, App	371	6	4.3	1346	2	US-08-470-566B-23	Sequence 23, Appl
299	6	4.3	711	4	US-09-134-001C-5460	Sequence 5460, Ap	372	6	4.3	1346	2	US-08-469-334-23	Sequence 23, Appl
300	6	4.3	729	4	US-09-252-991A-26827	Sequence 26827, A	373	6	4.3	1346	2	US-09-300-529-23	Sequence 23, Appl
301	6	4.3	731	2	US-08-911-364-1	Sequence 1, Appl	374	6	4.3	1394	3	US-09-213-053-2	Sequence 2, Appl
302	6	4.3	731	4	US-09-340-736E-1	Sequence 1, Appl	375	6	4.3	1418	4	US-09-252-991A-32367	Sequence 32367, A
303	6	4.3	733	3	US-08-464-700-2	Sequence 2, Appl	376	6	4.3	1422	4	US-08-469-260A-86	Sequence 86, Appl
304	6	4.3	740	1	US-08-257-073-5	Sequence 5, Appl	377	6	4.3	1422	4	US-08-488-446-86	Sequence 86, Appl
305	6	4.3	760	1	US-08-230-491A-2	Sequence 2, Appl	378	6	4.3	1422	4	US-08-467-344A-86	Sequence 86, Appl
306	6	4.3	760	1	US-08-619-280A-2	Sequence 2, Appl	379	6	4.3	1480	3	US-09-191-647-7	Sequence 7, Appl
307	6	4.3	760	2	US-08-940-391-2	Sequence 2, Appl	380	6	4.3	1480	3	US-09-540-245A-7	Sequence 7, Appl
308	6	4.3	776	2	US-08-700-607-5	Sequence 5, Appl	381	6	4.3	1480	3	US-09-340-153-7	Sequence 7, Appl
309	6	4.3	778	5	PCT-US93-03076-3	Sequence 3, Appl	382	6	4.3	1480	5	US-09-182-024A-5	Sequence 5, Appl
310	6	4.3	788	5	PCT-US93-03076-4	Sequence 4, Appl	383	6	4.3	1480	5	PCT-US91-09055-2	Sequence 2, Appl
311	6	4.3	792	2	US-08-678-039A-40	Sequence 40, Appl	384	6	4.3	1503	3	US-08-976-255-14	Sequence 14, Appl
312	6	4.3	798	3	US-09-150-460B-8	Sequence 8, Appl	385	6	4.3	1513	5	US-08-976-255-14	Sequence 2, Appl
313	6	4.3	805	4	US-09-252-991A-17822	Sequence 17822, A	386	6	4.3	1589	3	PCT-US93-03076-2	Sequence 2, Appl
314	6	4.3	824	4	US-09-252-991A-17822	Sequence 17822, A	387	6	4.3	1611	2	US-09-356-952-4	Sequence 4, Appl
315	6	4.3	851	4	US-09-252-991A-24773	Sequence 24773, A	388	6	4.3	1711	2	US-08-342-930-2	Sequence 2, Appl
316	6	4.3	858	3	US-07-956-483-17	Sequence 17, Appl	389	6	4.3	2523	1	US-08-185-432-18	Sequence 18, Appl
317	6	4.3	858	4	US-09-206-551-18	Sequence 18, Appl	390	6	4.3	2523	1	US-08-899-232-3	Sequence 3, Appl
318	6	4.3	873	1	US-08-571-758-6	Sequence 6, Appl	391	6	4.3	2556	3	US-08-083-590A-20	Sequence 20, Appl
319	6	4.3	873	1	US-08-909-984A-6	Sequence 6, Appl	392	6	4.3	2556	3	US-08-532-384-20	Sequence 20, Appl

393	6	4.3	3170	2	US-07-642-734C-5	Sequence 5, Appli	466	5	3.5	10	3	US-09-101-167-7	Sequence 7, Appli
394	6	4.3	3170	3	US-08-439-009A-5	Sequence 5, Appli	467	5	3.5	10	4	US-09-201-945-417	Sequence 417, App
395	6	4.3	3200	2	US-07-477-451-8	Sequence 8, Appli	468	5	3.5	11	1	US-08-268-251-30	Sequence 30, Appl
396	6	4.3	3201	4	US-09-679-279-15	Sequence 15, Appl	469	5	3.5	11	1	US-08-336-343A-23	Sequence 23, Appl
397	6	4.3	3246	4	US-09-679-279-13	Sequence 13, Appl	470	5	3.5	11	5	PCT-US93-01112-30	Sequence 30, Appl
398	6	4.3	3229	2	US-08-804-227C-4	Sequence 4, Appli	471	5	3.5	12	3	US-09-426-680-15	Sequence 15, Appl
399	6	4.3	4472	2	US-08-804-227C-2	Sequence 2, Appli	472	5	3.5	12	3	US-09-426-680-16	Sequence 16, Appl
400	6	4.3	4536	4	US-09-180-422B-27	Sequence 27, Appl	473	5	3.5	12	4	US-08-728-742A-49	Sequence 49, Appl
401	6	4.3	4545	2	US-08-804-227C-14	Sequence 14, Appl	474	5	3.5	13	1	US-07-895-300A-3	Sequence 3, Appli
402	6	4.3	4563	4	US-09-108-006C-1	Sequence 1, Appli	475	5	3.5	13	1	US-09-107-991-6	Sequence 6, Appli
403	6	4.3	6095	3	US-09-144-085-2	Sequence 2, Appli	476	5	3.5	13	3	US-09-638-112-3	Sequence 3, Appli
404	5	3.5	5	2	US-08-637-759B-303	Sequence 303, App	477	5	3.5	13	4	PCT-US93-05136-3	Sequence 3, Appli
405	5	3.5	5	3	US-08-871-355A-303	Sequence 303, App	478	5	3.5	13	5	PCT-US95-04121-28	Sequence 28, Appl
406	5	3.5	5	4	US-09-201-945-303	Sequence 303, App	479	5	3.5	13	5	US-08-232-453A-18	Sequence 18, Appl
407	5	3.5	6	1	US-08-403-718-5	Sequence 5, Appli	480	5	3.5	14	1	US-08-232-453A-27	Sequence 27, Appl
408	5	3.5	6	1	US-08-619-462-5	Sequence 5, Appli	481	5	3.5	14	1	US-08-232-453A-28	Sequence 28, Appl
409	5	3.5	6	6	5276016-1	Patent No. 5276016	482	5	3.5	14	1	US-08-232-453A-41	Sequence 41, Appl
410	5	3.5	7	3	US-09-173-941-32	Sequence 32, Appl	483	5	3.5	14	1	US-08-232-453A-44	Sequence 44, Appl
411	5	3.5	8	1	US-07-920-597-4	Sequence 4, Appli	484	5	3.5	14	1	US-08-179-632-16	Sequence 16, Appl
412	5	3.5	8	1	US-08-554-758-1	Sequence 1, Appli	485	5	3.5	14	1	US-08-179-632-19	Sequence 19, Appl
413	5	3.5	8	1	US-08-302-829-2	Sequence 2, Appli	486	5	3.5	14	1	US-08-179-632-19	Sequence 19, Appl
414	5	3.5	8	1	US-08-302-829-3	Sequence 3, Appli	487	5	3.5	14	1	US-08-440-174A-16	Sequence 16, Appl
415	5	3.5	8	1	US-08-302-829-5	Sequence 5, Appli	488	5	3.5	14	1	US-08-440-174A-19	Sequence 19, Appl
416	5	3.5	8	1	US-08-302-829-10	Sequence 10, Appl	489	5	3.5	14	3	US-09-120-365-81	Sequence 81, Appl
417	5	3.5	8	1	US-08-488-252-32	Sequence 32, Appl	490	5	3.5	14	3	US-09-515-019-81	Sequence 81, Appl
418	5	3.5	8	1	US-08-481-840A-1	Sequence 1, Appli	491	5	3.5	14	5	PCT-US91-07958-1	Sequence 1, Appli
419	5	3.5	8	1	US-08-481-840A-2	Sequence 2, Appli	492	5	3.5	14	5	PCT-US95-00062-16	Sequence 16, Appl
420	5	3.5	8	1	US-08-481-840A-3	Sequence 3, Appli	493	5	3.5	14	5	PCT-US95-00062-19	Sequence 19, Appl
421	5	3.5	8	1	US-08-403-718-1	Sequence 1, Appli	494	5	3.5	15	3	US-08-630-916A-105	Sequence 105, App
422	5	3.5	8	1	US-08-403-718-4	Sequence 4, Appli	495	5	3.5	15	3	US-08-041-889-20	Sequence 20, Appl
423	5	3.5	8	1	US-08-403-718-6	Sequence 6, Appli	496	5	3.5	15	3	US-08-837-058-20	Sequence 20, Appl
424	5	3.5	8	1	US-08-619-462-1	Sequence 1, Appli	497	5	3.5	15	3	US-08-481-190-11	Sequence 11, Appl
425	5	3.5	8	1	US-08-619-462-4	Sequence 4, Appli	498	5	3.5	15	3	US-08-481-190-12	Sequence 12, Appl
426	5	3.5	8	1	US-08-619-462-6	Sequence 6, Appli	499	5	3.5	15	3	US-08-602-999A-311	Sequence 311, App
427	5	3.5	8	2	US-08-540-412-12	Sequence 12, Appl	500	5	3.5	15	3	US-09-248-588-88	Sequence 88, Appl
428	5	3.5	8	2	US-08-117-187-2	Sequence 2, Appli	501	5	3.5	15	3	US-08-913-362-17	Sequence 17, Appl
429	5	3.5	8	2	US-08-598-873-42	Sequence 42, Appl	502	5	3.5	15	4	US-08-630-915A-161	Sequence 161, App
430	5	3.5	8	2	US-08-747-137-20	Sequence 20, Appl	503	5	3.5	15	4	US-09-500-124-311	Sequence 311, App
431	5	3.5	8	3	US-09-082-837A-3	Sequence 3, Appli	504	5	3.5	15	4	US-09-417-264-20	Sequence 20, Appl
432	5	3.5	8	3	US-09-082-837A-5	Sequence 5, Appli	505	5	3.5	15	4	US-09-073-009-67	Sequence 67, Appl
433	5	3.5	8	3	US-09-082-837A-10	Sequence 10, Appl	506	5	3.5	15	4	US-09-073-009-69	Sequence 69, Appl
434	5	3.5	8	3	US-09-051-342-12	Sequence 12, Appl	507	5	3.5	15	5	PCT-US93-00869-11	Sequence 11, Appl
435	5	3.5	8	3	US-09-051-759-12	Sequence 12, Appl	508	5	3.5	15	5	PCT-US93-00869-12	Sequence 12, Appl
436	5	3.5	8	3	US-08-605-430-42	Sequence 42, Appl	509	5	3.5	18	1	US-07-798-776-8	Sequence 8, Appli
437	5	3.5	8	3	US-09-421-845-2	Sequence 2, Appli	510	5	3.5	18	2	US-08-640-847C-7	Sequence 7, Appli
438	5	3.5	8	3	US-09-421-845-3	Sequence 3, Appli	511	5	3.5	18	3	US-08-251-288A-8	Sequence 8, Appli
439	5	3.5	8	3	US-09-421-845-5	Sequence 5, Appli	512	5	3.5	18	3	US-09-298-819A-8	Sequence 8, Appli
440	5	3.5	8	3	US-09-421-845-10	Sequence 10, Appl	513	5	3.5	19	1	US-08-036-555B-172	Sequence 172, App
441	5	3.5	8	6	5276016-2	Patent No. 5276016	514	5	3.5	19	1	US-08-469-569-172	Sequence 172, App
442	5	3.5	9	1	US-08-201-046A-29	Sequence 29, Appl	515	5	3.5	19	1	US-08-249-332A-172	Sequence 172, App
443	5	3.5	9	1	US-08-261-525A-4	Sequence 4, Appli	516	5	3.5	19	1	US-08-097-987A-7	Sequence 7, Appli
444	5	3.5	9	1	US-08-464-318-3	Sequence 3, Appli	517	5	3.5	19	1	US-08-463-526A-172	Sequence 172, App
445	5	3.5	9	2	US-08-471-341-3	Sequence 3, Appli	518	5	3.5	19	2	US-08-734-591A-172	Sequence 172, App
446	5	3.5	9	2	US-08-292-968-13	Sequence 13, Appl	519	5	3.5	19	2	US-08-469-660-172	Sequence 172, App
447	5	3.5	9	2	US-08-461-566-3	Sequence 3, Appli	520	5	3.5	19	3	US-08-341-018-74	Sequence 74, Appl
448	5	3.5	9	2	US-08-467-974-13	Sequence 13, Appl	521	5	3.5	19	3	US-08-665-574C-7	Sequence 7, Appli
449	5	3.5	9	2	US-08-467-974-13	Sequence 13, Appl	522	5	3.5	19	3	US-08-470-335-172	Sequence 172, App
450	5	3.5	9	2	US-08-467-974-13	Sequence 13, Appl	523	5	3.5	19	3	US-08-735-021-172	Sequence 172, App
451	5	3.5	9	3	US-08-467-974-13	Sequence 13, Appl	524	5	3.5	19	3	US-08-734-664A-172	Sequence 172, App
452	5	3.5	9	3	US-08-159-339A-792	Sequence 792, App	525	5	3.5	19	3	US-08-946-994-7	Sequence 7, Appli
453	5	3.5	10	1	US-08-082-514-13	Sequence 13, Appl	526	5	3.5	19	3	US-08-470-339-172	Sequence 172, App
454	5	3.5	10	1	US-08-166-195A-17	Sequence 17, Appl	527	5	3.5	19	3	US-09-184-938-9	Sequence 9, Appli
455	5	3.5	10	1	US-08-166-195A-18	Sequence 18, Appl	528	5	3.5	19	4	US-08-467-602-172	Sequence 172, App
456	5	3.5	10	1	US-08-395-443-1	Sequence 1, Appli	529	5	3.5	19	5	PCT-US94-05083C-168	Sequence 168, App
457	5	3.5	10	1	US-08-604-913B-2	Sequence 2, Appli	530	5	3.5	19	5	PCT-US95-06846A-172	Sequence 172, App
458	5	3.5	10	2	US-08-436-772-17	Sequence 17, Appl	531	5	3.5	20	1	US-07-678-974D-10	Sequence 10, Appl
459	5	3.5	10	2	US-08-436-772-18	Sequence 18, Appl	532	5	3.5	20	1	US-07-678-974D-10	Sequence 10, Appl
460	5	3.5	10	2	US-08-436-883B-17	Sequence 17, Appl	533	5	3.5	20	2	US-08-715-568A-13	Sequence 13, Appl
461	5	3.5	10	2	US-08-436-883B-18	Sequence 18, Appl	534	5	3.5	20	2	US-08-945-168-2	Sequence 2, Appli
462	5	3.5	10	2	US-08-637-759B-417	Sequence 417, App	535	5	3.5	20	2	US-08-945-168-15	Sequence 15, Appl
463	5	3.5	10	2	US-08-844-031-21	Sequence 21, Appl	536	5	3.5	20	2	US-08-945-168-40	Sequence 40, Appl
464	5	3.5	10	3	US-08-871-355A-417	Sequence 417, App	537	5	3.5	20	3	US-09-060-410-25	Sequence 25, Appl
465	5	3.5	10	3	US-08-159-339A-794	Sequence 794, App	538	5	3.5	20	4	US-07-946-180B-6	Sequence 6, Appli

539	5	3.5	20	4	US-09-723-458-25	Sequence 25, Appl	612	27	2	US-08-683-262B-19	Sequence 19, Appl
540	5	3.5	21	1	US-08-319-590-10	Sequence 10, Appl	613	27	2	US-09-005-069-8	Sequence 8, Appl
541	5	3.5	21	1	US-08-487-001A-10	Sequence 10, Appl	614	27	3	US-08-963-121C-9	Sequence 9, Appl
542	5	3.5	21	2	US-08-630-822A-10	Sequence 10, Appl	615	27	3	US-08-851-843A-114	Sequence 114, App
543	5	3.5	21	2	US-08-711-905-10	Sequence 10, Appl	616	27	3	US-08-974-549A-234	Sequence 234, App
544	5	3.5	21	2	US-09-005-069-10	Sequence 10, Appl	617	27	3	US-09-157-910-4	Sequence 4, Appl
545	5	3.5	21	4	US-09-004-730A-146	Sequence 146, App	618	27	3	US-09-361-707-19	Sequence 19, Appl
546	5	3.5	21	4	US-08-981-799A-146	Sequence 146, App	619	27	3	US-08-854-050-114	Sequence 114, App
547	5	3.5	22	4	US-09-288-143-125	Sequence 125, App	620	27	3	US-09-543-513-9	Sequence 9, Appl
548	5	3.5	22	1	US-08-093-383-25	Sequence 25, Appl	621	27	4	US-09-430-323-114	Sequence 114, App
549	5	3.5	23	1	US-08-179-632-17	Sequence 17, Appl	622	27	4	US-08-912-951-115	Sequence 115, App
550	5	3.5	23	1	US-08-319-590-7	Sequence 7, Appl	623	27	4	US-09-004-730A-144	Sequence 144, App
551	5	3.5	23	1	US-08-440-174A-17	Sequence 17, Appl	624	27	4	US-08-981-799A-144	Sequence 144, App
552	5	3.5	23	1	US-08-487-001A-7	Sequence 7, Appl	625	27	5	PCT-US95-04803-10	Sequence 10, Appl
553	5	3.5	23	2	US-08-482-142-71	Sequence 71, Appl	626	28	1	US-08-179-632-10	Sequence 10, Appl
554	5	3.5	23	2	US-08-630-822A-7	Sequence 7, Appl	627	28	1	US-08-440-174A-10	Sequence 10, Appl
555	5	3.5	23	2	US-08-711-905-7	Sequence 7, Appl	628	28	3	US-08-486-099-87	Sequence 87, Appl
556	5	3.5	23	2	US-09-005-069-7	Sequence 7, Appl	629	28	3	US-08-360-107A-97	Sequence 97, Appl
557	5	3.5	23	2	US-08-478-572-71	Sequence 71, Appl	630	28	3	US-08-484-223B-87	Sequence 87, Appl
558	5	3.5	23	2	US-08-484-286-71	Sequence 71, Appl	631	28	3	US-08-919-597-87	Sequence 87, Appl
559	5	3.5	23	4	US-09-004-730A-143	Sequence 143, App	632	28	3	US-08-475-668A-87	Sequence 87, Appl
560	5	3.5	23	4	US-08-981-799A-143	Sequence 143, App	633	28	3	US-08-485-551A-87	Sequence 87, Appl
561	5	3.5	23	5	PCT-US95-00062-17	Sequence 17, Appl	634	28	3	US-08-471-913A-87	Sequence 87, Appl
562	5	3.5	24	2	US-08-482-142-148	Sequence 148, App	635	28	3	US-08-485-264A-87	Sequence 87, Appl
563	5	3.5	24	2	US-08-482-142-148	Sequence 148, App	636	28	4	US-08-474-349A-87	Sequence 87, Appl
564	5	3.5	24	2	US-08-478-572-148	Sequence 148, App	637	28	4	US-08-255-208A-23	Sequence 23, Appl
565	5	3.5	24	2	US-08-478-572-149	Sequence 149, App	638	28	4	US-08-470-896-87	Sequence 87, Appl
566	5	3.5	24	2	US-08-706-209-5	Sequence 5, Appl	639	28	4	US-08-485-546A-87	Sequence 87, Appl
567	5	3.5	24	2	US-08-706-209-6	Sequence 6, Appl	640	28	5	PCT-US95-00062-10	Sequence 10, Appl
568	5	3.5	24	2	US-08-706-209-7	Sequence 7, Appl	641	29	1	US-07-794-288D-180	Sequence 180, App
569	5	3.5	24	2	US-08-706-209-8	Sequence 8, Appl	642	29	1	US-08-179-632-11	Sequence 11, Appl
570	5	3.5	24	3	US-08-981-787-2	Sequence 2, Appl	643	30	1	US-08-179-632-12	Sequence 12, Appl
571	5	3.5	24	3	US-08-860-300-6	Sequence 6, Appl	644	30	1	US-08-440-174A-11	Sequence 11, Appl
572	5	3.5	24	3	US-08-860-300-7	Sequence 7, Appl	645	30	1	US-08-440-174A-12	Sequence 12, Appl
573	5	3.5	24	3	US-08-860-300-8	Sequence 8, Appl	646	30	1	US-09-184-021-8	Sequence 8, Appl
574	5	3.5	24	3	US-08-860-300-9	Sequence 9, Appl	647	30	3	US-09-184-021-8	Sequence 8, Appl
575	5	3.5	24	3	US-08-484-296-148	Sequence 148, App	648	30	5	PCT-US95-00062-11	Sequence 11, Appl
576	5	3.5	24	3	US-08-484-296-149	Sequence 149, App	649	30	5	PCT-US95-00062-12	Sequence 12, Appl
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578	5	3.5	24	4	US-09-489-847-269	Sequence 269, App	651	31	5	US-08-440-174A-2	Sequence 2, Appl
579	5	3.5	24	4	US-08-981-861-3	Sequence 3, Appl	652	31	5	PCT-US95-00062-2	Sequence 2, Appl
580	5	3.5	24	4	US-08-981-861-4	Sequence 4, Appl	653	32	2	US-08-452-075-2	Sequence 2, Appl
581	5	3.5	24	5	PCT-US95-16596-6	Sequence 6, Appl	654	32	3	US-08-452-075-2	Sequence 2, Appl
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583	5	3.5	24	5	PCT-US95-16596-8	Sequence 8, Appl	656	32	4	US-08-817-335-3	Sequence 3, Appl
584	5	3.5	24	5	PCT-US95-16596-9	Sequence 9, Appl	657	34	3	US-09-397-680A-4	Sequence 4, Appl
585	5	3.5	24	5	PCT-US96-11373-3	Sequence 3, Appl	658	34	4	US-08-467-602-188	Sequence 188, App
586	5	3.5	24	5	PCT-US96-11374-3	Sequence 3, Appl	659	34	4	US-09-205-258-309	Sequence 309, App
587	5	3.5	24	5	PCT-US96-11374-3	Sequence 3, Appl	660	34	4	US-09-690-454-208	Sequence 208, App
588	5	3.5	24	5	PCT-US96-11375-2	Sequence 2, Appl	661	35	3	US-08-851-843A-178	Sequence 178, App
589	5	3.5	24	6	5424193-1	Patent No. 5424199	662	35	3	US-08-974-549A-297	Sequence 297, App
590	5	3.5	25	1	US-08-366-690-2	Sequence 2, Appl	663	35	3	US-08-854-050-178	Sequence 178, App
591	5	3.5	26	1	US-08-036-555B-128	Sequence 128, App	664	35	4	US-09-430-323-178	Sequence 178, App
592	5	3.5	26	1	US-08-469-569-128	Sequence 128, App	665	35	4	US-09-227-357-183	Sequence 183, App
593	5	3.5	26	1	US-07-942-245-216	Sequence 216, App	666	35	4	US-08-319-590-9	Sequence 9, Appl
594	5	3.5	26	1	US-07-942-245-334	Sequence 334, App	667	35	4	US-08-487-001A-9	Sequence 9, Appl
595	5	3.5	26	1	US-07-942-245-408	Sequence 408, App	668	36	2	US-08-630-822A-9	Sequence 9, Appl
596	5	3.5	26	1	US-08-249-322A-128	Sequence 128, App	669	36	2	US-08-711-905-9	Sequence 9, Appl
597	5	3.5	26	1	US-08-427-072-10	Sequence 10, Appl	670	36	2	US-09-005-069-9	Sequence 9, Appl
598	5	3.5	26	1	US-08-469-526A-128	Sequence 128, App	671	36	4	US-09-004-730A-145	Sequence 145, App
599	5	3.5	26	2	US-08-734-591A-128	Sequence 128, App	672	36	4	US-08-981-799A-145	Sequence 145, App
600	5	3.5	26	2	US-08-469-660-128	Sequence 128, App	673	37	3	US-08-814-052-37	Sequence 37, Appl
601	5	3.5	26	3	US-08-470-335-128	Sequence 128, App	674	37	3	US-08-812-829-29	Sequence 29, Appl
602	5	3.5	26	3	US-08-735-021-128	Sequence 128, App	675	37	3	US-08-578-674-6	Sequence 6, Appl
603	5	3.5	26	3	US-08-734-664A-128	Sequence 128, App	676	37	3	US-09-498-346-6	Sequence 6, Appl
604	5	3.5	26	4	US-08-470-339-128	Sequence 128, App	677	37	3	US-08-349-403-4	Sequence 4, Appl
605	5	3.5	26	4	US-08-467-602-128	Sequence 128, App	678	38	2	US-08-448-481-7	Sequence 7, Appl
606	5	3.5	26	5	PCT-US94-05083C-124	Sequence 124, App	679	40	1	US-08-179-632-3	Sequence 3, Appl
607	5	3.5	26	5	PCT-US95-06846A-128	Sequence 128, App	680	40	1	US-08-179-632-4	Sequence 4, Appl
608	5	3.5	27	1	US-08-319-590-8	Sequence 8, Appl	681	40	1	US-08-179-632-5	Sequence 5, Appl
609	5	3.5	27	1	US-08-487-001A-8	Sequence 8, Appl	682	40	1	US-08-440-174A-3	Sequence 3, Appl
610	5	3.5	27	2	US-08-630-822A-8	Sequence 8, Appl	683	40	1	US-08-440-174A-4	Sequence 4, Appl
611	5	3.5	27	2	US-08-711-905-8	Sequence 8, Appl	684	40	1	US-08-440-174A-5	Sequence 5, Appl

685	5	3.5	40	5	PCT-US95-00062-3	Sequence 3, Appli	758	5	3.5	59	3	US-08-470-339-199	Sequence 199, App
686	5	3.5	40	5	PCT-US95-00062-4	Sequence 4, Appli	759	5	3.5	59	3	US-09-300-672-8	Sequence 8, Appli
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688	5	3.5	41	4	US-07-946-180B-7	Sequence 7, Appli	761	5	3.5	59	4	US-08-467-602-405	Sequence 405, App
689	5	3.5	41	4	US-09-904-615-96	Sequence 96, Appli	762	5	3.5	60	4	US-09-015-030-9	Sequence 9, Appli
690	5	3.5	42	3	US-08-341-018-30	Sequence 30, Appli	763	5	3.5	60	4	US-09-381-546-13	Sequence 13, Appli
691	5	3.5	42	3	US-08-470-335-214	Sequence 214, App	764	5	3.5	62	4	US-08-735-021-188	Sequence 188, App
692	5	3.5	42	3	US-08-470-339-214	Sequence 214, App	765	5	3.5	62	4	US-07-946-180B-9	Sequence 9, Appli
693	5	3.5	42	4	US-08-467-602-211	Sequence 211, App	766	5	3.5	63	4	US-08-871-924A-2	Sequence 2, Appli
694	5	3.5	42	4	US-08-467-602-408	Sequence 408, App	767	5	3.5	63	4	US-09-361-800-2	Sequence 2, Appli
695	5	3.5	43	1	US-07-956-700B-66	Sequence 66, Appli	768	5	3.5	63	4	US-10-097-777-2	Sequence 40, Appli
696	5	3.5	43	1	US-08-476-537-66	Sequence 66, Appli	769	5	3.5	63	4	US-09-367-895-40	Sequence 42, App
697	5	3.5	43	1	US-08-485-607-66	Sequence 66, Appli	770	5	3.5	64	1	US-09-328-352-4931	Sequence 22, Appli
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726	5	3.5	51	4	US-08-936-165A-282	Sequence 282, App	799	5	3.5	72	3	US-08-946-329A-108	Sequence 108, App
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749	5	3.5	56	3	US-09-498-346-16	Sequence 16, App	822	5	3.5	78	4	US-09-328-352-4322	Sequence 4322, Ap
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751	5	3.5	56	6	5496550-10	Patent No. 5496550	824	5	3.5	80	4	US-09-732-210-312	Sequence 312, App
752	5	3.5	58	3	US-08-341-018-16	Sequence 16, Appli	825	5	3.5	81	4	US-09-732-210-312	Sequence 25, Appli
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755	5	3.5	58	4	US-08-467-602-208	Sequence 208, App	828	5	3.5	82	2	US-08-624-123-6	Sequence 6, Appli
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757	5	3.5	59	3	US-08-470-335-199	Sequence 199, App	830	5	3.5	83	4	US-09-252-991A-27556	Sequence 27556, A
												US-09-732-210-1197	Sequence 1197, Ap

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833	5	3.5	84	3	US-09-498-346-2	Sequence 2, Appl	906	5	3.5	106	4	US-09-134-001C-4025	Sequence 4025, Ap
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835	5	3.5	86	4	US-09-996-243-274	Sequence 274, App	908	5	3.5	108	4	US-09-328-352-5869	Sequence 5869, Ap
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837	5	3.5	88	2	US-08-751-767A-54	Sequence 54, Appl	910	5	3.5	109	1	US-08-271-252-4	Sequence 4, Appl
838	5	3.5	88	4	US-08-936-165A-287	Sequence 287, App	911	5	3.5	109	1	US-08-448-198A-1	Sequence 1, Appl
839	5	3.5	88	4	US-09-219-983A-1	Sequence 1, Appl	912	5	3.5	109	4	US-09-341-444A-2	Sequence 2, Appl
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849	5	3.5	90	1	US-08-168-091A-32	Sequence 32, Appl	922	5	3.5	112	3	US-08-873-970-78	Sequence 78, Appl
850	5	3.5	90	4	US-09-489-847-204	Sequence 204, App	923	5	3.5	112	3	US-09-095-855-78	Sequence 78, Appl
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852	5	3.5	90	4	US-09-107-532A-4309	Sequence 4309, App	925	5	3.5	112	4	US-09-205-426-78	Sequence 78, Appl
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855	5	3.5	92	4	US-09-178-176B-10	Sequence 10, Appl	928	5	3.5	113	3	US-08-406-030A-29	Sequence 29, Appl
856	5	3.5	92	4	US-09-457-864-10	Sequence 10, Appl	929	5	3.5	113	4	US-09-004-730A-101	Sequence 101, App
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858	5	3.5	93	1	US-08-326-117B-5	Sequence 5, Appl	931	5	3.5	113	4	US-09-081-799A-101	Sequence 101, App
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862	5	3.5	93	4	US-09-205-258-703	Sequence 703, App	935	5	3.5	115	3	US-09-153-733A-19	Sequence 19, Appl
863	5	3.5	93	4	US-09-252-991A-24991	Sequence 24991, A	936	5	3.5	115	3	US-08-946-092A-17	Sequence 17, Appl
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871	5	3.5	94	3	US-09-557-917-98	Sequence 98, Appl	944	5	3.5	115	5	PCT-US94-00685-17	Sequence 17, Appl
872	5	3.5	94	4	US-09-252-991A-32861	Sequence 32861, A	945	5	3.5	116	1	US-08-581-529B-15	Sequence 15, Appl
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875	5	3.5	95	1	US-08-742-035-23	Sequence 23, Appl	948	5	3.5	116	2	US-08-581-528A-15	Sequence 15, Appl
876	5	3.5	95	2	US-08-777-019-23	Sequence 23, Appl	949	5	3.5	116	3	US-09-041-889-38	Sequence 38, Appl
877	5	3.5	95	2	US-08-777-143-23	Sequence 23, Appl	950	5	3.5	116	3	US-09-097-616-15	Sequence 15, Appl
878	5	3.5	95	3	US-08-775-414-23	Sequence 23, Appl	951	5	3.5	116	3	US-09-177-860A-25	Sequence 25, Appl
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881	5	3.5	95	3	US-08-981-739-23	Sequence 23, Appl	954	5	3.5	116	4	US-09-378-238-35	Sequence 35, Appl
882	5	3.5	95	4	US-09-387-418A-21	Sequence 21, Appl	955	5	3.5	116	4	US-09-629-938-25	Sequence 25, Appl
883	5	3.5	95	4	US-09-128-026-23	Sequence 23, Appl	956	5	3.5	116	4	US-09-417-264-38	Sequence 38, Appl
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886	5	3.5	96	2	US-08-446-363-7	Sequence 7, Appl	959	5	3.5	116	5	PCT-US94-00657-21	Sequence 21, Appl
887	5	3.5	96	3	US-09-258-373-22	Sequence 22, Appl	960	5	3.5	116	5	PCT-US94-0762-15	Sequence 15, Appl
888	5	3.5	96	4	US-09-252-991A-22796	Sequence 22796, A	961	5	3.5	116	5	PCT-US94-07799-15	Sequence 15, Appl
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890	5	3.5	97	4	US-09-252-991A-30054	Sequence 30054, A	963	5	3.5	117	3	US-09-255-953-7	Sequence 7, Appl
891	5	3.5	98	1	US-08-211-202-140	Sequence 140, App	964	5	3.5	117	3	US-09-046-479-2	Sequence 2, Appl
892	5	3.5	98	4	US-09-134-001C-4233	Sequence 4233, Ap	965	5	3.5	117	4	US-08-525-539A-76	Sequence 76, Appl
893	5	3.5	98	4	US-09-198-452A-57	Sequence 57, Appl	966	5	3.5	117	4	US-08-858-207A-453	Sequence 453, App
894	5	3.5	99	3	US-08-931-858E-170	Sequence 170, App	967	5	3.5	117	4	US-08-822-897C-2	Sequence 2, Appl
895	5	3.5	99	3	US-08-981-739-170	Sequence 170, App	968	5	3.5	117	4	US-09-608-810A-4	Sequence 4, Appl
896	5	3.5	99	4	US-09-128-026-170	Sequence 170, App	969	5	3.5	117	4	US-09-872-090-7	Sequence 7, Appl
897	5	3.5	100	4	US-09-107-532A-6916	Sequence 6916, Ap	970	5	3.5	117	4	US-09-996-243-268	Sequence 268, App
898	5	3.5	102	3	US-09-142-469-6	Sequence 6, Appl	971	5	3.5	117	4	US-09-745-032-7	Sequence 7, Appl
899	5	3.5	102	4	US-09-101-751A-90	Sequence 90, Appl	972	5	3.5	118	3	US-09-214-214A-5	Sequence 5, Appl
900	5	3.5	103	3	US-09-041-889-39	Sequence 39, Appl	973	5	3.5	118	3	US-09-255-953-5	Sequence 5, Appl
901	5	3.5	103	4	US-09-417-264-39	Sequence 39, Appl	974	5	3.5	118	4	US-09-101-751A-46	Sequence 46, Appl
902	5	3.5	104	4	US-09-230-485-5	Sequence 5, Appl	975	5	3.5	118	4	US-08-872-090-5	Sequence 5, Appl
903	5	3.5	104	4	US-09-230-485-7	Sequence 7, Appl	976	5	3.5	118	4	US-09-745-032-5	Sequence 5, Appl

977 5 3.5 118 4 US-09-252-991A-16780 Sequence 16780, A
978 5 3.5 119 1 US-07-979-630-3 Sequence 3, Appl
979 5 3.5 119 1 US-07-634-278-64 Sequence 64, Appl
980 5 3.5 119 1 US-08-477-728-64 Sequence 64, Appl
981 5 3.5 119 1 US-08-474-040-64 Sequence 64, Appl
982 5 3.5 119 1 US-08-487-200-64 Sequence 64, Appl
983 5 3.5 119 1 US-08-440-049-2 Sequence 2, Appl
984 5 3.5 119 1 US-08-340-131-3 Sequence 3, Appl
985 5 3.5 119 2 US-08-441-513A-2 Sequence 2, Appl
986 5 3.5 119 3 US-08-970-865-5 Sequence 5, Appl
987 5 3.5 119 3 US-08-910-691-12 Sequence 12, Appl
988 5 3.5 119 3 US-08-581-662-2 Sequence 2, Appl
989 5 3.5 119 3 US-08-484-537-64 Sequence 64, Appl
990 5 3.5 119 3 US-09-363-573-5 Sequence 5, Appl
991 5 3.5 119 3 US-09-214-214A-6 Sequence 6, Appl
992 5 3.5 119 3 US-09-036-574-2 Sequence 2, Appl
993 5 3.5 119 3 US-09-253-953-6 Sequence 6, Appl
994 5 3.5 119 4 US-09-025-769B-21 Sequence 21, Appl
995 5 3.5 119 4 US-08-845-541B-2 Sequence 2, Appl
996 5 3.5 119 4 US-09-187-789-21 Sequence 21, Appl
997 5 3.5 119 4 US-09-066-065A-2 Sequence 2, Appl
998 5 3.5 119 4 US-09-664-295-2 Sequence 2, Appl
999 5 3.5 119 4 US-09-139-600-16 Sequence 16, Appl
1000 5 3.5 119 4 US-09-872-090-6 Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-09-230-041-42
; Sequence 42, Application US/09230041A
; Patent No. 6465179
; GENERAL INFORMATION:
; APPLICANT: THIREOS, GEORGE
; APPLICANT: KAPETZOPOULOS, DIMITRIS
; TITLE OF INVENTION: DNA ENCODING AN ARTHROPOD CHITIN SYNTHASE
; FILE REFERENCE: DNA ENCODING AN ARTHROPOD CHITIN SYNTH
; CURRENT APPLICATION NUMBER: US/09/230,041A
; CURRENT FILING DATE: 1999-01-19
; EARLIER APPLICATION NUMBER: EP97108240.9
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Rhizobium leguminosarum
US-09-230-041-42

Query Match 5.0%; Score 7; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 SAIAATV 65
Db 10 SAIAATV 16
|||||

RESULT 2

US-09-230-041-37
; Sequence 37, Application US/09230041A
; Patent No. 6465179
; GENERAL INFORMATION:
; APPLICANT: THIREOS, GEORGE
; APPLICANT: KAPETZOPOULOS, DIMITRIS
; TITLE OF INVENTION: DNA ENCODING AN ARTHROPOD CHITIN SYNTHASE
; FILE REFERENCE: DNA ENCODING AN ARTHROPOD CHITIN SYNTH
; CURRENT APPLICATION NUMBER: US/09/230,041A
; CURRENT FILING DATE: 1999-01-19
; EARLIER APPLICATION NUMBER: EP97108240.9
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Rhizobium leguminosarum
US-09-230-041-37

Query Match 5.0%; Score 7; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 SAIAATV 65
Db 10 SAIAATV 16
|||||

RESULT 3

US-09-384-302A-8
; Sequence 8, Application US/09384302A
; Patent No. 6451543
; GENERAL INFORMATION:
; APPLICANT: Kochendoerfer, Gerd G
; APPLICANT: Hunter, Christie L
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Botti, Paolo
; APPLICANT: Gryphon Sciences
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis
; FILE REFERENCE: gfrn-028/02WO
; CURRENT APPLICATION NUMBER: US/09/384,302A
; CURRENT FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/144,964
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 09/263,971
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-384-302A-8

Query Match 5.0%; Score 7; DB 4; Length 293;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 189 VLPGTGA 195
|||||

RESULT 4

US-09-325-932A-190
; Sequence 190, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325,932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 190
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-325-932A-190

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Query Match      5.0%; Score 7; DB 4; Length 320;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      126 FRLRLS 132
      |||||
Db      252 FRLRLS 258

RESULT 5
US-08-671-525B-8
; Sequence 8, Application US/08671525B
; Patent No. 5703220
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/671,525B
; FILING DATE: June 27, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-671-525B-8

Query Match      5.0%; Score 7; DB 1; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      52 VLPGTGA 58
      |||||
Db      228 VLPGTGA 234

RESULT 6
US-08-672-109B-8
; Sequence 8, Application US/08672109B
; Patent No. 5710265
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,045
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-672-109B-8

Query Match      5.0%; Score 7; DB 1; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      52 VLPGTGA 58
      |||||
Db      228 VLPGTGA 234

RESULT 7
US-08-842-045-8
; Sequence 8, Application US/08842045
; Patent No. 5817787
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,045
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-842-045-8
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Query Match      5.0%; Score 7; DB 1; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      52 VLPGTGA 58
      |||||
Db      228 VLPGTGA 234

RESULT 7
US-08-842-045-8
; Sequence 8, Application US/08842045
; Patent No. 5817787
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,045
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-672-109B-8

Query Match      5.0%; Score 7; DB 1; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      52 VLPGTGA 58
      |||||
Db      228 VLPGTGA 234

RESULT 7
US-08-842-045-8
; Sequence 8, Application US/08842045
; Patent No. 5817787
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Ira
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,045
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVE
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-672-109B-8
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US-08-842-045-8

Query Match 5.0%; Score 7; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPQTGA 58
| | | | |
DB 228 VLPQTGA 234

RESULT 8

US-08-842-238-8
; Sequence 8, Application US/08842238
; Patent No. 5869257
; GENERAL INFORMATION:
; APPLICANT: Yamada, Tadataka
; APPLICANT: Gantz, Iza
; TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS: 23
; ADDRESSEE: Hainres, Dickey & Pierce, P.L.C.
; STREET: P.O. Box 828
; CITY: Bloomfield Hills
; STATE: MI
; COUNTRY: US
; ZIP: 48303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,238
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, Deann F.
; REGISTRATION NUMBER: 36683
; REFERENCE/DOCKET NUMBER: 2115-000853DVD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810)641-1600
; TELEFAX: (810)641-0270
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-842-238-8

Query Match 5.0%; Score 7; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPQTGA 58
| | | | |
DB 228 VLPQTGA 234

RESULT 9

US-08-662-560-2
; Sequence 2, Application US/08662560
; Patent No. 5908609
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Wei, Gu
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS
; USEFUL IN THE REGULATION OF BODY WEIGHT
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,560
FILING DATE: 10-JUN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-060
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-662-560-2

Query Match 5.0%; Score 7; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPQTGA 58
| | | | |
DB 228 VLPQTGA 234

RESULT 10

US-08-780-749A-2
; Sequence 2, Application US/08780749A
; Patent No. 5932779
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS
; USEFUL IN THE REGULATION OF BODY WEIGHT
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,749A
; FILING DATE: 08-JAN-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Laura A. Coruzzi

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-064
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-780-749A-2

Query Match 5.0%; Score 7; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 11
US-08-780-749A-6
Sequence 6, Application US/08780749A
Patent No. 5932779
GENERAL INFORMATION:
APPLICANT: Lee, Frank
APPLICANT: Huszar, Dennis
APPLICANT: Gu, Wei
TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS
TITLE OF INVENTION: USEFUL IN THE REGULATION OF BODY WEIGHT
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036/2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,749A
FILING DATE: 08-JAN-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Laura A. Coruzzi
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-064
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-780-749A-6

Query Match 5.0%; Score 7; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-064
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-780-749A-2

Query Match 5.0%; Score 7; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 12
US-08-706-281A-16
Sequence 16, Application US/08706281A
Patent No. 6100048
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
APPLICANT: Fan, Wei
APPLICANT: Kesterton, Robert A
APPLICANT: Lu, Dongsi
APPLICANT: Chen, Wenbiao
TITLE OF INVENTION: Methods and Reagents for Discovering and
TITLE OF INVENTION: Using Mammalian Melanocortin Receptor Agonists and Antagonist
TITLE OF INVENTION: To Modulate Feeding Behavior in Animals
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/706,281A
FILING DATE: 04-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 6100048nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-706-281A-16

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 13
US-08-629-335B-8
Sequence 8, Application US/08629335B
Patent No. 6117975
GENERAL INFORMATION:
APPLICANT: Yamada, Tadataka
APPLICANT: Gantz, Ira
TITLE OF INVENTION: Genes Encoding Melanocortin Receptors
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Harness, Dickey & Pierce, P.L.C.
STREET: P.O. Box 828
CITY: Bloomfield Hills

STATE: MI
COUNTRY: US
ZIP: 48303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/629,335B
APPLICATION NUMBER: US/08/629,335B
FILING DATE: July 23, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, DeAnn F.
REGISTRATION NUMBER: 36683
REFERENCE/DOCKET NUMBER: 2115-000853DVA
TELEPHONE: (810)641-1600
TELEFAX: (810)641-0270
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids
TYPE: amino acid
MOLECULE TYPE: linear
US-08-629-335B-8

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 14
US-09-097-231-16
Sequence 16, Application US/09097231
Patent No. 6278038
GENERAL INFORMATION:
APPLICANT: Cone, Roger D
Low, Malcolm J
Chen, Wenbiao
TITLE OF INVENTION: Mammalian Melanocortin Receptor and Uses
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,231
FILING DATE: 12-Jun-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: No. 6278038nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 96,886-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 332 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-097-231-16

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 15
US-08-870-511-2
Sequence 2, Application US/08870511
Patent No. 6287763
GENERAL INFORMATION:
APPLICANT: Lee, Frank
APPLICANT: Huszar, Dennis
APPLICANT: Gu, Wei
TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
FILE REFERENCE: 7853-083
CURRENT APPLICATION NUMBER: US/08/870,511
CURRENT FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 332
TYPE: PRT
ORGANISM: Homo sapiens
US-08-870-511-2

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 16
US-08-870-511-6
Sequence 6, Application US/08870511
Patent No. 6287763
GENERAL INFORMATION:
APPLICANT: Lee, Frank
APPLICANT: Huszar, Dennis
APPLICANT: Gu, Wei
TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
FILE REFERENCE: 7853-083
CURRENT APPLICATION NUMBER: US/08/870,511
CURRENT FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 332
TYPE: PRT
ORGANISM: Homo sapiens
US-08-870-511-6

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 17
US-08-870-511-8
; Sequence 8, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-870-511-8

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 18
US-08-870-511-10
; Sequence 10, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-083
; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-870-511-10

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 19
US-08-870-511-12
; Sequence 12, Application US/08870511
; Patent No. 6287763
; GENERAL INFORMATION:
; APPLICANT: Lee, Frank
; APPLICANT: Huszar, Dennis
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL IN THE
; TITLE OF INVENTION: REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-083

; CURRENT APPLICATION NUMBER: US/08/870,511
; CURRENT FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-870-511-12

Query Match 5.0%; Score 7; DB 3; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 20
US-09-384-302A-6
; Sequence 6, Application US/09384302A
; Patent No. 6451543
; GENERAL INFORMATION:
; APPLICANT: Kochendoerfer, Gerd G
; APPLICANT: Hunter, Christie L
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Botti, Paolo
; APPLICANT: Gryphon Sciences
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis
; TITLE OF INVENTION: of Membrane Polypeptides
; FILE REFERENCE: grfn-028/02WO
; CURRENT APPLICATION NUMBER: US/09/384,302A
; CURRENT FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/144,964
; PRIOR FILING DATE: 1998-08-31
; PRIOR APPLICATION NUMBER: 09/263,971
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-384-302A-6

Query Match 5.0%; Score 7; DB 4; Length 332;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 21
US-09-384-302A-9
; Sequence 9, Application US/09384302A
; Patent No. 6451543
; GENERAL INFORMATION:
; APPLICANT: Kochendoerfer, Gerd G
; APPLICANT: Hunter, Christie L
; APPLICANT: Kent, Stephen B.H.
; APPLICANT: Botti, Paolo
; APPLICANT: Gryphon Sciences
; TITLE OF INVENTION: Lipid Matrix-Assisted Chemical Ligation and Synthesis
; TITLE OF INVENTION: of Membrane Polypeptides
; FILE REFERENCE: grfn-028/02WO
; CURRENT APPLICATION NUMBER: US/09/384,302A
; CURRENT FILING DATE: 1999-08-26
; PRIOR APPLICATION NUMBER: 09/144,964

; PRIOR FILING DATE: 1998-08-31
 ; PRIOR APPLICATION NUMBER: 09/263,971
 ; PRIOR FILING DATE: 1999-03-05
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 332
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-384-302A-9

Query Match 5.0%; Score 7; DB 4; Length 332;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
 Db 228 VLPGTGA 234

RESULT 22
 US-09-353-099-16
 ; Sequence 16, Application US/09353099
 ; Patent No. 6476187
 ; GENERAL INFORMATION:
 ; APPLICANT: Cone, Roger D
 ; Fan, Wei
 ; Boston, Bruce A
 ; Kesterton, Robert A
 ; Lu, Dongxi
 ; Chen, Wenbiao

TITLE OF INVENTION: Methods and Reagents for Discovering and
 Using Mammalian Melanocortin Receptor Agonists and Antagonists
 To Modulate Feeding Behavior in Animals

NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
 STREET: 300 South Wacker Drive
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/353,099
 FILING DATE: 14-Sep-1999
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/706,281
 FILING DATE: 04-SEP-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 6476187ran, Kevin E
 REGISTRATION NUMBER: 35,303
 REFERENCE/DOCKET NUMBER: 96,886
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-913-0001
 TELEFAX: 312-913-0002
 TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 332 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 16:

US-09-353-099-16

Query Match 5.0%; Score 7; DB 4; Length 332;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
 Db 228 VLPGTGA 234

RESULT 23
 US-09-831-206-2
 ; Sequence 2, Application US/09831206
 ; Patent No. 6573070
 ; GENERAL INFORMATION:
 ; APPLICANT: MacNeil, Douglas J.
 ; APPLICANT: Weinberg, David H.
 ; APPLICANT: Van der Ploeg, Leonardus H. T.

TITLE OF INVENTION: DNA MOLECULES ENCODING THE MELANOCORTIN
 4 RECEPTOR PROTEIN FROM RHESUS MONKEY
 FILE REFERENCE: 20190P
 CURRENT APPLICATION NUMBER: US/09/831,206
 CURRENT FILING DATE: 2001-06-28
 PRIOR APPLICATION NUMBER: PCT/US99/25767
 PRIOR FILING DATE: 1999-11-05
 PRIOR APPLICATION NUMBER: 60/107,721
 PRIOR FILING DATE: 1998-11-09
 NUMBER OF SEQ ID NOS: 6
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 332
 TYPE: PRT
 ORGANISM: rhesus monkey (Macaca mulatta)
 US-09-831-206-2

Query Match 5.0%; Score 7; DB 4; Length 332;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
 Db 228 VLPGTGA 234

RESULT 24
 US-09-252-991A-29610
 ; Sequence 29610, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 29610
 LENGTH: 341
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-29610

Query Match 5.0%; Score 7; DB 4; Length 341;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ERLAMLR 42
 Db 90 ERLAMLR 96

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; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6840

Query Match      5.0%; Score 7; DB 4; Length 522;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      55 GTGASAI 61
Db      211 GTGASAI 217

RESULT 28
US-09-328-352-6683
; Sequence 6683, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6683
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6683

Query Match      5.0%; Score 7; DB 4; Length 525;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      55 GTGASAI 61
Db      201 GTGASAI 207

RESULT 29
US-09-252-991A-23068
; Sequence 23068, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23068
; LENGTH: 538
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23068

Query Match      5.0%; Score 7; DB 4; Length 538;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      55 GTGASAI 61
Db      209 GTGASAI 215

RESULT 30
US-08-268-251-19
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31144

Query Match      5.0%; Score 7; DB 4; Length 354;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      36 ERLAMLR 42
Db      327 ERLAMLR 333

RESULT 26
US-09-328-352-6474
; Sequence 6474, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6474
; LENGTH: 516
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6474

Query Match      5.0%; Score 7; DB 4; Length 516;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      55 GTGASAI 61
Db      202 GTGASAI 208

RESULT 27
US-09-328-352-6840
; Sequence 6840, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6840
; LENGTH: 522
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```

; Sequence 19, Application US/08268251
; Patent No. 5595475
; GENERAL INFORMATION:
; APPLICANT: Jamieson, Gordon A
; APPLICANT: Dedman, John R
; APPLICANT: Kaetzel, Marcia A
; TITLE OF INVENTION: Calmodulin-Binding Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,251
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/831,219
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D
; REGISTRATION NUMBER: 31,259
; REFERENCE/DOCKET NUMBER: 272.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-268-251-19

Query Match 4.3%; Score 6; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 LRSLSK 134
DB 7 LRSLSK 12

RESULT 31
PCT-US93-01112-19
; Sequence 19, Application PC/TUS9301112
; GENERAL INFORMATION:
; APPLICANT: Jamieson, Gordon A
; APPLICANT: Dedman, John R
; APPLICANT: Kaetzel, Marcia A
; TITLE OF INVENTION: Calmodulin-Binding Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1

```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01112
; FILING DATE: 19930208
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 07/831,219
; APPLICATION NUMBER:
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D
; REGISTRATION NUMBER: 31,259
; REFERENCE/DOCKET NUMBER: 272.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-01112-19

Query Match 4.3%; Score 6; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 LRSLSK 134
DB 7 LRSLSK 12

RESULT 32
US-09-203-258-1217
; Sequence 1217, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893

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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1217
; TYPE: PRT
; LENGTH: 20
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-205-258-1217

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Query Match 4.3%; Score 6; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 132 LKSGGV 137
Db 1 LKSGGV 6

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RESULT 33
US-08-268-251-49
; Sequence 49, Application US/08268251
; Patent No. 5585475
; GENERAL INFORMATION:
; APPLICANT: Jamieson, Gordon A
; APPLICANT: Dedman, John R

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; APPLICANT: Kaetzel, Marcia A
; TITLE OF INVENTION: Calmodulin-Binding Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/268,251
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/831,219
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D
; REGISTRATION NUMBER: 31,259
; REFERENCE/DOCKET NUMBER: 272.001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 601-2706
; TELEFAX: (510) 655-3542
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-268-251-49

Query Match 4.3%; Score 6; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 LRSLSK 134
Db 9 LRSLSK 14

RESULT 34
PCT-US93-01112-49
; Sequence 49, Application PC/TUS9301112
; GENERAL INFORMATION:
; APPLICANT: Jamieson, Gordon A
; APPLICANT: Dedman, John R
; APPLICANT: Kaetzel, Marcia A
; TITLE OF INVENTION: Calmodulin-Binding Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/01112
; FILING DATE: 19930208
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: US 07/831,219
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 272.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2706
TELEFAX: (510) 658-3542
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-01112-49

Query Match 4.3%; Score 6; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 LRLSKS 134
Db 9 LRLSKS 14

RESULT 35
US-08-658-136-38
Sequence 38, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W
APPLICANT: LANDES, GREGORY M
APPLICANT: BURN, TIMOTHY C
APPLICANT: CONNORS, TIMOTHY D
APPLICANT: DACKOWSKI, WILLIAM
APPLICANT: GERMINO, GREGORY
APPLICANT: OLAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENZYME CORPORATION
STREET: ONE MOUNTAIN ROAD
CITY: FRAMINGHAM
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,136
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, ELIZABETH
REGISTRATION NUMBER: 31,845
REFERENCE/DOCKET NUMBER: GEN4-17.8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-658-136-38

Query Match 4.3%; Score 6; DB 3; Length 34;

Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 127 RHLRSL 132
Db 2 RHLRSL 7

RESULT 36
US-08-179-632-8
Sequence 8, Application US/08179632
Patent No. 5607914
GENERAL INFORMATION:
APPLICANT: Rao, A. Gururaj; Zhong, Lingxiu
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International, Inc.
STREET: 700 Capital Square, 400 Locust Street
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/Microsoft Windows
SOFTWARE: Microsoft Windows No. 5607914epad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,632
FILING DATE: 07-JAN-1994
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 08/079,512
FILING DATE: 06/18/93
ATTORNEY/AGENT INFORMATION:
NAME: Roth, Michael J.
REGISTRATION NUMBER: 29,342
REFERENCE/DOCKET NUMBER: 0233 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 245-3594
TELEFAX: (515) 245-3634
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-179-632-8

Query Match 4.3%; Score 6; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 LRALAG 46
Db 21 LRALAG 26

RESULT 37
US-08-440-174A-8
Sequence 8, Application US/08440174A
Patent No. 5717061
GENERAL INFORMATION:
APPLICANT: Rao, Gururaj A.
APPLICANT: Zhong, Lingxiu
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: PIONEER HI-BRED INTERNATIONAL, INC.
STREET: 7100 N.W. 62nd Avenue
CITY: Johnston

STATE: Iowa
COUNTRY: USA
ZIP: 50131
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,174A
FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/079,512
FILING DATE: 18-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bobrowicz, Donna
REGISTRATION NUMBER: 32,196
REFERENCE/DOCKET NUMBER: 0234R2D-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4896
TELEFAX: (515) 334-6883
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-440-174A-8

Query Match 4.3%; Score 6; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 41 LRALAG 46
DB 21 LRALAG 26

RESULT 39
PCT-US95-00062-8
Sequence 8, Application PC/TUS9500062
GENERAL INFORMATION:
APPLICANT: Pioneer Hi-Bred International, Inc.
TITLE OF INVENTION: SYNTHETIC ANTIMICROBIAL PEPTIDES
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International, Inc.
STREET: 700 Capital Square, 400 Locust Street
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/Microsoft Windows
SOFTWARE: Microsoft Windows Notepad
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00062
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Yates, Michael E.; Sweeney, Patricia A.;
NAME: Roth, Michael J.; & Simon, Soma G.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 234R2-PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800

TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-00062-8

Query Match 4.3%; Score 6; DB 5; Length 41;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 6; Conservative 0; Mismatches 0; Indels 0;

QY 41 LRALAG 46
DB 21 LRALAG 26

RESULT 39
US-09-205-258-1215
Sequence 1215, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
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EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1215
LENGTH: 55
TYPE: PRT
ORGANISM: Homo sapiens
US-09-205-258-1215

Query Match 4.3%; Score 6; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 132 LKSGV 137
Db 15 LKSGV 20

RESULT 40
US-09-134-001C-2886
Sequence 2886, Application US/09134001C
Patent No. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 2886
LENGTH: 63
TYPE: PRT
ORGANISM: Staphylococcus epidermidis

US-09-134-001C-2886
Query Match 4.3%; Score 6; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 35 LPGTGA 40
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Job time : 52 secs

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Run on: November 14, 2003, 10:52:17 ; Search time 30 Seconds
(without alignments)
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Title: US-10-087-573-2
Perfect score: 141
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	126	89.4	285	12	US-10-087-573-4
3	8	5.7	467	15	US-10-156-761-11753
4	7	5.0	16	15	US-10-225-567A-1062
5	7	5.0	32	12	US-10-179-382-42
6	7	5.0	35	12	US-10-179-382-37
7	5.0	320	15	US-10-219-220-190	Sequence 190, App
8	7	5.0	332	12	US-10-318-661-27
9	7	5.0	332	12	US-10-373-355-2
10	7	5.0	332	12	US-10-413-752-2
11	7	5.0	332	12	US-10-413-752-6
12	7	5.0	332	15	US-10-288-160-16
13	7	5.0	332	15	US-10-074-754-2
14	7	5.0	332	15	US-10-225-567A-158
15	7	5.0	338	9	US-09-815-242-11881

16	5.0	469	10	US-09-866-582-10	Sequence 10, Appl
17	5.0	520	15	US-10-156-761-11162	Sequence 1162, A
18	5.0	699	15	US-10-128-714-3468	Sequence 3468, Ap
19	5.0	748	9	US-09-815-242-10278	Sequence 10278, A
20	5.0	808	15	US-10-128-714-8468	Sequence 8468, Ap
21	5.0	1029	15	US-10-156-761-11059	Sequence 11059, A
22	4.3	9	10	US-09-779-308-211	Sequence 211, App
23	4.3	9	10	US-09-824-787B-135	Sequence 135, App
24	4.3	10	10	US-09-779-308-63	Sequence 63, Appl
25	4.3	11	12	US-10-105-232-305	Sequence 305, App
26	4.3	11	12	US-10-105-232-340	Sequence 340, App
27	4.3	11	12	US-10-189-437-292	Sequence 292, App
28	4.3	11	12	US-10-189-437-327	Sequence 327, App
29	4.3	12	12	US-10-105-232-339	Sequence 339, App
30	4.3	12	12	US-10-189-437-326	Sequence 326, App
31	4.3	13	11	US-09-992-665-13	Sequence 13, Appl
32	4.3	20	12	US-09-933-767-1217	Sequence 1217, Ap
33	4.3	20	15	US-10-023-282-1217	Sequence 1217, Ap
34	4.3	20	15	US-10-115-072-33	Sequence 33, Appl
35	4.3	21	12	US-10-105-232-303	Sequence 303, App
36	4.3	21	12	US-10-189-437-290	Sequence 290, App
37	4.3	22	12	US-10-105-232-302	Sequence 302, App
38	4.3	22	12	US-10-189-437-289	Sequence 289, App
39	4.3	23	9	US-09-864-761-47718	Sequence 47718, A
40	4.3	23	12	US-10-105-232-301	Sequence 301, App
41	4.3	23	12	US-10-189-437-288	Sequence 288, App
42	4.3	27	12	US-10-105-232-337	Sequence 337, App
43	4.3	27	12	US-10-189-437-324	Sequence 324, App
44	4.3	34	9	US-09-864-761-34841	Sequence 34841, A
45	4.3	45	9	US-09-864-761-41437	Sequence 41437, A
46	4.3	51	9	US-09-864-761-41437	Sequence 41437, A
47	4.3	52	9	US-09-864-761-40064	Sequence 40064, A
48	4.3	52	9	US-09-864-761-34357	Sequence 34357, A
49	4.3	55	10	US-09-764-877-1185	Sequence 1185, Ap
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51	4.3	55	15	US-10-023-282-1215	Sequence 1215, Ap
52	4.3	62	11	US-09-764-891-3750	Sequence 3750, Ap
53	4.3	69	10	US-09-796-692-1250	Sequence 1250, Ap
54	4.3	69	10	US-09-796-692-1716	Sequence 1716, Ap
55	4.3	69	10	US-09-796-692-2017	Sequence 2017, Ap
56	4.3	69	10	US-09-796-692-2259	Sequence 2259, Ap
57	4.3	69	15	US-10-040-862-1250	Sequence 1250, Ap
58	4.3	69	15	US-10-040-862-1716	Sequence 1716, Ap
59	4.3	69	15	US-10-040-862-2017	Sequence 2017, Ap
60	4.3	69	15	US-10-040-862-2259	Sequence 2259, Ap
61	4.3	71	10	US-09-894-882-125	Sequence 125, App
62	4.3	75	10	US-10-128-714-8326	Sequence 8326, Ap
63	4.3	77	11	US-09-910-009A-35	Sequence 35, Appl
64	4.3	78	11	US-09-910-009A-38	Sequence 38, Appl
65	4.3	79	12	US-10-231-417-312	Sequence 312, App
66	4.3	81	12	US-10-029-386-31353	Sequence 31353, A
67	4.3	83	12	US-10-029-386-30631	Sequence 30631, A
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713	6	4.3	183	10	US-09-895-9138-330	Sequence 330, App	786	6	4.3	250	11	US-09-880-748-78	Sequence 78, Appl
714	6	4.3	184	12	US-10-127-032-95	Sequence 95, Appl	787	6	4.3	250	11	US-09-880-748-80	Sequence 80, Appl
715	6	4.3	189	10	US-09-738-626-5353	Sequence 5353, Ap	788	6	4.3	250	11	US-09-880-748-81	Sequence 81, Appl
716	6	4.3	190	10	US-09-764-864-1252	Sequence 1252, Ap	789	6	4.3	250	11	US-09-880-748-82	Sequence 82, Appl
717	6	4.3	200	9	US-09-137-531-20	Sequence 20, Appl	790	6	4.3	251	11	US-09-880-748-100	Sequence 100, App
718	6	4.3	201	10	US-09-764-864-1561	Sequence 1561, Ap	791	6	4.3	251	11	US-09-880-748-140	Sequence 140, App
719	6	4.3	203	10	US-09-738-626-4228	Sequence 4228, Ap	792	6	4.3	251	11	US-09-880-748-9	Sequence 9, Appl
720	6	4.3	209	9	US-09-815-242-5452	Sequence 5452, Ap	793	6	4.3	251	11	US-09-880-748-10	Sequence 10, Appl
721	6	4.3	209	9	US-09-815-242-12382	Sequence 12382, Ap	794	6	4.3	251	11	US-09-880-748-11	Sequence 11, Appl
722	6	4.3	209	9	US-09-998-481-39	Sequence 39, Appl	795	6	4.3	251	11	US-09-880-748-12	Sequence 12, Appl
723	6	4.3	211	12	US-09-815-242-12980	Sequence 12980, A	796	6	4.3	251	11	US-09-880-748-13	Sequence 13, Appl
724	6	4.3	216	10	US-09-764-846-210	Sequence 210, App	797	6	4.3	251	11	US-09-880-748-14	Sequence 14, Appl
725	6	4.3	216	15	US-10-091-483-210	Sequence 210, App	798	6	4.3	251	11	US-09-880-748-15	Sequence 15, Appl
726	6	4.3	216	15	US-10-156-761-14056	Sequence 14056, A	799	6	4.3	251	11	US-09-880-748-16	Sequence 16, Appl
727	6	4.3	217	9	US-09-764-853-664	Sequence 664, App	800	6	4.3	251	11	US-09-880-748-17	Sequence 17, Appl
728	6	4.3	219	10	US-09-993-737-130	Sequence 130, App	801	6	4.3	251	11	US-09-880-748-18	Sequence 18, Appl
729	6	4.3	221	9	US-09-728-914-4	Sequence 4, Appl	802	6	4.3	251	11	US-09-880-748-19	Sequence 19, Appl
730	6	4.3	227	15	US-10-156-761-11914	Sequence 11914, A	803	6	4.3	251	11	US-09-880-748-20	Sequence 20, Appl
731	6	4.3	227	15	US-10-156-761-13766	Sequence 13766, A	804	6	4.3	251	11	US-09-880-748-21	Sequence 21, Appl
732	6	4.3	228	15	US-10-156-761-8437	Sequence 8437, Ap	805	6	4.3	251	11	US-09-880-748-22	Sequence 22, Appl
733	6	4.3	231	10	US-09-738-626-5162	Sequence 5162, Ap	806	6	4.3	251	11	US-09-880-748-23	Sequence 23, Appl
734	6	4.3	231	15	US-10-156-761-7876	Sequence 7876, Ap	807	6	4.3	251	11	US-09-880-748-24	Sequence 24, Appl
735	6	4.3	232	15	US-10-156-761-11422	Sequence 11422, A	808	6	4.3	251	11	US-09-880-748-25	Sequence 25, Appl
736	6	4.3	242	11	US-09-880-748-1830	Sequence 1830, Ap	809	6	4.3	251	11	US-09-880-748-26	Sequence 26, Appl
737	6	4.3	242	11	US-09-880-748-1844	Sequence 1844, Ap	810	6	4.3	251	11	US-09-880-748-27	Sequence 27, Appl
738	6	4.3	243	11	US-09-880-748-1515	Sequence 1515, Ap	811	6	4.3	251	11	US-09-880-748-28	Sequence 28, Appl
739	6	4.3	243	11	US-09-880-748-1533	Sequence 1533, Ap	812	6	4.3	251	11	US-09-880-748-29	Sequence 29, Appl
740	6	4.3	244	11	US-09-880-748-1863	Sequence 1863, Ap	813	6	4.3	251	11	US-09-880-748-30	Sequence 30, Appl
741	6	4.3	244	11	US-09-880-748-1124	Sequence 1124, Ap	814	6	4.3	251	11	US-09-880-748-31	Sequence 31, Appl
742	6	4.3	244	11	US-09-880-748-1491	Sequence 1491, Ap	815	6	4.3	251	11	US-09-880-748-32	Sequence 32, Appl
743	6	4.3	244	11	US-09-880-748-1498	Sequence 1498, Ap	816	6	4.3	251	11	US-09-880-748-33	Sequence 33, Appl
744	6	4.3	244	11	US-09-880-748-1524	Sequence 1524, Ap	817	6	4.3	251	11	US-09-880-748-34	Sequence 34, Appl
745	6	4.3	244	11	US-09-880-748-1568	Sequence 1568, Ap	818	6	4.3	251	11	US-09-880-748-35	Sequence 35, Appl
												US-09-880-748-37	Sequence 37, Appl


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US-10-156-761-11753

Query Match      5.7%; Score 8; DB 15; Length 467;
Best Local Similarity 100.0%; Pred. No. 21;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      55 GTGASATA 62
      |||||
Db      413 GTGASATA 420

RESULT 4
US-10-225-567A-1062
; Sequence 1062, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1062
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1062

Query Match      5.0%; Score 7; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      52 VLPGTGA 58
      |||||
Db      5 VLPGTGA 11

RESULT 5
US-10-179-382-42
; Sequence 42, Application US/10179382
; Publication No. US20030166235A1
; GENERAL INFORMATION:
; APPLICANT: THIREOS, GEORGE
; APPLICANT: KAPETZOPOULOS, DIMITRIS
; TITLE OF INVENTION: DNA ENCODING AN ARTHROPOD CHITIN SYNTHASE
; FILE REFERENCE: DNA ENCODING AN ARTHROPOD CHITIN SYNTH
; CURRENT APPLICATION NUMBER: US/10/179,382
; CURRENT FILING DATE: 2002-06-26
; PRIOR APPLICATION NUMBER: US/09/230,041
; PRIOR FILING DATE: 1999-01-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 42
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Rhizobium leguminosarum
US-10-179-382-42

Query Match      5.0%; Score 7; DB 12; Length 32;
Best Local Similarity 100.0%; Pred. No. 18;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      59 SAATAATV 65
      |||||
Db      10 SAATAATV 16

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; PRIOR APPLICATION NUMBER: US 09/341,446
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US97/05334
; PRIOR FILING DATE: 1997-03-25
; PRIOR APPLICATION NUMBER: US 08/622,349
; PRIOR FILING DATE: 1996-03-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-318-661-27

Query Match 5.0%; Score 7; DB 12; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 9
US-10-373-355-2
; Sequence 2, Application US/10373355
; Publication No. US20030166009A1
; GENERAL INFORMATION:
; APPLICANT: MacNeill, Douglas J.
; APPLICANT: Weinberg, David H.
; APPLICANT: Van der Ploeg, Leonardus H. T.
; TITLE OF INVENTION: DNA MOLECULES ENCODING THE MELANOCORTIN
; TITLE OF INVENTION: 4 RECEPTOR PROTEIN FROM RHESUS MONKEY
; FILE REFERENCE: 20190P
; CURRENT APPLICATION NUMBER: US/10/373,355
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: US/09/831,206
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/US99/25767
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 60/107,721
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: rhesus monkey (Macaca mulatta)
US-10-373-355-2

Query Match 5.0%; Score 7; DB 12; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 10
US-10-413-752-2
; Sequence 2, Application US/10413752
; Publication No. US20030171295A1
; GENERAL INFORMATION:
; APPLICANT: Frank Lee
; APPLICANT: Dennis Huszar
; APPLICANT: Wei Gu
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL
; TITLE OF INVENTION: IN THE REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-145
; CURRENT APPLICATION NUMBER: US/10/413,752
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/322,695

; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/662,560
; PRIOR FILING DATE: 1996-06-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-413-752-2

Query Match 5.0%; Score 7; DB 12; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 11
US-10-413-752-6
; Sequence 6, Application US/10413752
; Publication No. US20030171295A1
; GENERAL INFORMATION:
; APPLICANT: Frank Lee
; APPLICANT: Dennis Huszar
; APPLICANT: Wei Gu
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL
; TITLE OF INVENTION: IN THE REGULATION OF BODY WEIGHT
; FILE REFERENCE: 7853-145
; CURRENT APPLICATION NUMBER: US/10/413,752
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: US/09/322,695
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 08/662,560
; PRIOR FILING DATE: 1996-06-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Rattus sp.
US-10-413-752-6

Query Match 5.0%; Score 7; DB 12; Length 332;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 12
US-10-288-160-16
; Sequence 16, Application US/10288160
; Publication No. US20030105024A1
; GENERAL INFORMATION:
; APPLICANT: Cone, Roger D
; APPLICANT: Fan, Wei
; APPLICANT: Boston, Bruce A
; APPLICANT: Kesterton, Robert A
; APPLICANT: Lu, Dongxi
; APPLICANT: Chen, Wenbiao
; TITLE OF INVENTION: Methods and Reagents for Discovering and
; Using Mammalian Melanocortin Receptor Agonists and Antagon
; To Modulate Feeding Behavior in Animals
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago

```
; STATE: IL
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/288,160
; FILING DATE: 05-NO. US20030105024A1-2002
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/706,281
; FILING DATE: 04-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. US20030105024A1nan, Kevin E
; REGISTRATION NUMBER: 35,303
; REFERENCE/DOCKET NUMBER: 96,886
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 332 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-288-160-16

Query Match 5.0%; Score 7; DB 15; Length 332;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 15
US-09-815-242-11881
; Sequence 11881, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11881
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11881

Query Match 5.0%; Score 7; DB 9; Length 338;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 14
US-10-225-567A-158

; Sequence 158, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 158
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-158

Query Match 5.0%; Score 7; DB 15; Length 332;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 13
US-10-074-754-2
; Sequence 2, Application US/10074754
; Publication No. US20030113263A1
; GENERAL INFORMATION:
; APPLICANT: Marks, Daniel L.
; APPLICANT: Cone, Roger D.
; TITLE OF INVENTION: Methods and Reagents for Discovering and Using
; TITLE OF INVENTION: Mammalian Melanocortin Receptor Antagonists to Treat
; TITLE OF INVENTION: Cachexia
; FILE REFERENCE: 96-886
; CURRENT APPLICATION NUMBER: US/10/074,754
; CURRENT FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 2
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-754-2

Query Match 5.0%; Score 7; DB 15; Length 332;
Best Local Similarity 100.0%; Pred.No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 VLPGTGA 58
Db 228 VLPGTGA 234

RESULT 14
US-10-225-567A-158
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```
QY 36 ERLAMLR 42
Db 311 ERLAMLR 317

RESULT 16
US-09-866-582-10
; Sequence 10, Application US/09866582
; Patent No. US20020127620A1
; GENERAL INFORMATION:
; APPLICANT: Witman, George B.
; APPLICANT: Fazour, Gregory J.
; APPLICANT: Rosenbaum, Joel L.
; APPLICANT: Cole, Douglas G.
; TITLE OF INVENTION: INTRACELLULAR TRANSPORT
; FILE REFERENCE: 07917-145001
; CURRENT APPLICATION NUMBER: US/09/866,582
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/206,923
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Chlamydomonas reinhardtii
US-09-866-582-10

Query Match 5.0%; Score 7; DB 10; Length 469;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 PGTGASA 60
Db 260 PGTGASA 266

RESULT 17
US-10-156-761-11162
; Sequence 11162, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 11162
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-11162

Query Match 5.0%; Score 7; DB 15; Length 520;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 GTGASAI 61
Db 193 GTGASAI 199

RESULT 18
US-10-128-714-3468
; Sequence 3468, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Hu, Wenqi
; APPLICANT: Tishkoff, Daniel
; APPLICANT: Zamudio, Carlos
; APPLICANT: Eroshkin, Alexey M
; APPLICANT: Lemieux, Sebastien M
; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
; TITLE OF INVENTION: Methods of Use
; FILE REFERENCE: 10182-018-999
; CURRENT APPLICATION NUMBER: US/10/128,714
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: US 60/285,697
; PRIOR FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: US 60/287,066
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/295,890
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/303,899
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/316,362
; PRIOR FILING DATE: 2001-08-31
; NUMBER OF SEQ ID NOS: 8603
; SOFTWARE: Patentln version 3.1
; SEQ ID NO 3468
; LENGTH: 699
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-128-714-3468

Query Match 5.0%; Score 7; DB 15; Length 699;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 STKSPEL 87
Db 336 STKSPEL 342

RESULT 19
US-09-815-242-10278
; Sequence 10278, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Hascibek, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
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; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10278
 ; LENGTH: 748
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 US-09-815-242-10278

Query Match 5.0%; Score 7; DB 9; Length 748;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 AMLRALA 45
 DB 646 AMLRALA 652

RESULT 20

US-10-128-714-8468
 ; Sequence 8468, Application US/10128714
 ; Publication No. US20030119013A1
 ; GENERAL INFORMATION:

; APPLICANT: Jiang, Bo
 ; APPLICANT: Tishkoff, Daniel
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Eroshkin, Alexey M
 ; APPLICANT: Lemieux, Sebastien M
 ; TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
 ; FILE REFERENCE: 10182-018-999
 ; CURRENT APPLICATION NUMBER: US/10/128,714
 ; PRIOR FILING DATE: 2002-04-23
 ; PRIOR APPLICATION NUMBER: US 60/285,697
 ; PRIOR FILING DATE: 2001-04-23
 ; PRIOR APPLICATION NUMBER: US 60/287,066
 ; PRIOR FILING DATE: 2001-04-27
 ; PRIOR APPLICATION NUMBER: US 60/295,890
 ; PRIOR FILING DATE: 2001-06-05
 ; PRIOR APPLICATION NUMBER: US 60/303,899
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: US 60/316,362
 ; PRIOR FILING DATE: 2001-08-31
 ; NUMBER OF SEQ ID NOS: 8603
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8468
 ; LENGTH: 808
 ; TYPE: PRT
 ; ORGANISM: Aspergillus fumigatus
 US-10-128-714-8468

Query Match 5.0%; Score 7; DB 15; Length 808;
 Best Local Similarity 100.0%; Pred. No. 3.3e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 81 STKGPEL 87
 DB 445 STKGPEL 451

RESULT 21

US-10-156-761-11059
 ; Sequence 11059, Application US/10156761
 ; Publication No. US20030119018A1
 ; GENERAL INFORMATION:
 ; APPLICANT: OMURA, SATOSHI
 ; APPLICANT: IKEDA, HARUO
 ; APPLICANT: ISHIKAWA, JUN
 ; APPLICANT: HORIKAWA, HIROSHI
 ; APPLICANT: SHIBA, TADAYOSHI

; APPLICANT: SAKAKI, YOSHIYUKI
 ; APPLICANT: HATTORI, MASAHIRA
 ; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 ; FILE REFERENCE: 249-262
 ; CURRENT APPLICATION NUMBER: US/10/156,761
 ; CURRENT FILING DATE: 2002-05-29
 ; PRIOR APPLICATION NUMBER: JP 2001-204089
 ; PRIOR FILING DATE: 2001-05-30
 ; PRIOR APPLICATION NUMBER: JP 2001-272697
 ; PRIOR FILING DATE: 2001-08-02
 ; NUMBER OF SEQ ID NOS: 15109
 ; SEQ ID NO 11059
 ; LENGTH: 1029
 ; TYPE: PRT
 ; ORGANISM: Streptomyces avermitilis
 US-10-156-761-11059

Query Match 5.0%; Score 7; DB 15; Length 1029;
 Best Local Similarity 100.0%; Pred. No. 4.1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 PGTGASA 60
 DB 92 PGTGASA 98

RESULT 22

US-09-779-308-211
 ; Sequence 211, Application US/09779308
 ; Patent No. US20020150972A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mary Paris
 ; APPLICANT: Daniel E.H. Afar
 ; APPLICANT: Pia M. Challita-Eid
 ; APPLICANT: Rene S. Hubert
 ; APPLICANT: Eliana Levin
 ; APPLICANT: Steve Chappell Mitchell
 ; APPLICANT: Aya Jakobovits
 ; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN
 ; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
 ; FILE REFERENCE: 129.4USU1
 ; CURRENT APPLICATION NUMBER: US/09/779,308
 ; CURRENT FILING DATE: 2001-02-08
 ; PRIOR APPLICATION NUMBER: 60/181,020
 ; PRIOR FILING DATE: 2000-02-08
 ; NUMBER OF SEQ ID NOS: 718
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 211
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-09-779-308-211

Query Match 4.3%; Score 6; DB 10; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSQ 136
 DB 3 SLKSQ 8

RESULT 23

US-09-824-787B-135
 ; Sequence 135, Application US/09824787B
 ; Patent No. US20020155447A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zauderer, Maurice
 ; APPLICANT: Evans, Elizabeth E.
 ; APPLICANT: Borrello, Melinda A.
 ; TITLE OF INVENTION: A Gene Differentially Expressed in Breast and
 ; TITLE OF INVENTION: Bladder Cancer, and Encoded Polypeptides
 ; FILE REFERENCE: 1821.0040001

; CURRENT APPLICATION NUMBER: US/09/824,787B
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/194,463
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-824-787B-135

Query Match 4.3%; Score 6; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 6e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 LPGTGA 58
Db 1 LPGTGA 6

RESULT 24
US-09-779-308-63

; Sequence 63, Application US/09779308
; Patent No. US20020150972A1

; GENERAL INFORMATION:

; APPLICANT: Mary Faris

; APPLICANT: Daniel E.H. Afar

; APPLICANT: Pia M. Challita-Eid

; APPLICANT: Rene S. Hubert

; APPLICANT: Elana Levin

; APPLICANT: Steve Chappell Mitchell

; APPLICANT: Ava Jakobovics

; TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN

; TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER

; FILE REFERENCE: 129.4USU1

; CURRENT APPLICATION NUMBER: US/09/779,308

; CURRENT FILING DATE: 2001-02-08

; PRIOR APPLICATION NUMBER: 60/181,020

; PRIOR FILING DATE: 2000-02-08

; NUMBER OF SEQ ID NOS: 718

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 63

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

US-09-779-308-63

Query Match 4.3%; Score 6; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSQ 136
Db 4 SLKSQ 9

RESULT 25

US-10-105-232-305

; Sequence 305, Application US/10105232

; Publication No. US20030180328A1

; GENERAL INFORMATION:

; APPLICANT: BOGOCH, SAMUEL

; APPLICANT: BOGOCH, ELENORE S.

; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS

; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS

; FILE REFERENCE: 09425-46904

; CURRENT APPLICATION NUMBER: US/10/105,232

; CURRENT FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: 60/303,396

; PRIOR FILING DATE: 2001-07-09

; PRIOR APPLICATION NUMBER: 60/278,761

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 305
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-105-232-305

Query Match 4.3%; Score 6; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSQ 136
Db 4 SLKSQ 9

RESULT 26

US-10-105-232-340

; Sequence 340, Application US/10105232

; Publication No. US20030180328A1

; GENERAL INFORMATION:

; APPLICANT: BOGOCH, SAMUEL

; APPLICANT: BOGOCH, ELENORE S.

; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS

; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS

; FILE REFERENCE: 09425-46904

; CURRENT APPLICATION NUMBER: US/10/105,232

; CURRENT FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: 60/303,396

; PRIOR FILING DATE: 2001-07-09

; PRIOR APPLICATION NUMBER: 60/278,761

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: 09/146,755

; PRIOR FILING DATE: 1998-09-04

; PRIOR APPLICATION NUMBER: 09/817,144

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: 08/198,139

; PRIOR FILING DATE: 1994-02-17

; NUMBER OF SEQ ID NOS: 535

; SOFTWARE: PatentIn 2.1

; SEQ ID NO 340

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Plasmodium falciparum

US-10-105-232-340

Query Match 4.3%; Score 6; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSQ 136
Db 5 SLKSQ 10

RESULT 27

US-10-189-437-292

; Sequence 292, Application US/10189437

; Publication No. US2003019441A1

; GENERAL INFORMATION:

; APPLICANT: BOGOCH, SAMUEL

; APPLICANT: BOGOCH, ELENORE S.

; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE

; FILE REFERENCE: 09425/46905

; CURRENT APPLICATION NUMBER: US/10/189,437

; CURRENT FILING DATE: 2002-07-08

```

; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 292
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-189-437-292

```

```

Query Match      4.3%; Score 6; DB 12; Length 11;
Best Local Similarity 100.0%; Pred.No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      131 SLKSQ 136
Db      4 SLKSQ 9

```

```

RESULT 28
US-10-189-437-327
; Sequence 327, Application US/10189437
; Publication No. US2003019441A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 327
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-189-437-327

```

```

Query Match      4.3%; Score 6; DB 12; Length 11;
Best Local Similarity 100.0%; Pred.No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      131 SLKSQ 136
Db      5 SLKSQ 10

```

```

RESULT 29
US-10-105-232-339
; Sequence 339, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26

```

```

; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 339
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-105-232-339

```

```

Query Match      4.3%; Score 6; DB 12; Length 12;
Best Local Similarity 100.0%; Pred.No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      131 SLKSQ 136
Db      6 SLKSQ 11

```

```

RESULT 30
US-10-189-437-326
; Sequence 326, Application US/10189437
; Publication No. US2003019441A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 326
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-189-437-326

```

```

Query Match      4.3%; Score 6; DB 12; Length 12;
Best Local Similarity 100.0%; Pred.No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      131 SLKSQ 136
Db      6 SLKSQ 11

```

```

RESULT 31
US-09-992-665-13
; Sequence 13, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kaja Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665

```

```

; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-13

Query Match      4.3%  Score 6;  DB 11;  Length 13;
Best Local Similarity 100.0%; Pred.No. 73;
Matches      6;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

QY      117 PLEKRR 122
Db      4 PLEKRR 9

RESULT 32
US-09-933-767-1217
; Sequence 1217, Application US/09933767
; Publication No. US20030181692A1
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P2
; CURRENT APPLICATION NUMBER: US/09/933,767
; CURRENT FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: PCT/US01/05614
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/184,836
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/193,170
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 09/205,258
; PRIOR FILING DATE: 1998-12-04
; PRIOR APPLICATION NUMBER: PCT/US98/11422
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/048,885
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,375
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,881
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,880
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,896
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,020
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,876
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,895
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,884
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,894
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,971
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,882
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,899
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,893
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,900

; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,901
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,892
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,915
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,019
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,972
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,916
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,373
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,875
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/049,374
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,917
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,949
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,962
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,963
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,877
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/048,878
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,054
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,064
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/068,053
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/070,923
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/073,160
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,159
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,165
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/073,164
; PRIOR FILING DATE: 1998-01-30
; PRIOR APPLICATION NUMBER: 60/085,925
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,921
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,923
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/085,922
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/092,921
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: 60/094,657
; PRIOR FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1245
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1217
; LENGTH: 20
```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-933-767-1217

Query Match
Best Local Similarity 4.3%; Score 6; DB 12; Length 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 LKSGQV 137
Db 1 LKSGQV 6

RESULT 33
US-10-023-282-1217
; Sequence 1217, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/10/023,282
; EARLIER FILING DATE: 2001-12-20
; EARLIER APPLICATION NUMBER: 09/205,258
; EARLIER FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-023-282-1217

Query Match
Best Local Similarity 4.3%; Score 6; DB 15; Length 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 LKSGQV 137
Db 1 LKSGQV 6

RESULT 34
US-10-115-072-33
; Sequence 33, Application US/10115072
; Publication No. US20030105003A1
; GENERAL INFORMATION:
; APPLICANT: NILSSON, JAN
; APPLICANT: SHAH, PREDIMAN K.
; TITLE OF INVENTION: PEPTIDE-BASED IMMUNIZATION THERAPY FOR TREATMENT OF
; TITLE OF INVENTION: ATHEROSCLEROSIS AND DEVELOPMENT OF PEPTIDE-BASED ASSAY
; TITLE OF INVENTION: FOR DETERMINATION OF IMMUNE RESPONSES AGAINST OXIDIZED
; TITLE OF INVENTION: LOW DENSITY LIPOPROTEIN
; FILE REFERENCE: 03940.0057
; CURRENT APPLICATION NUMBER: US/10/115,072
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/281,410
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: SE 0101232-7
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: SE 0103754-8
; PRIOR FILING DATE: 2001-09-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 20

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; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: peptide
 ; US-10-115-072-33

Query Match 4.3%; Score 6; DB 15; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 69 GASKML 74
 Db 2 GASKML 7

RESULT 35
 US-10-105-232-303
 ; Sequence 303, Application US/10105232
 ; Publication No. US20030180328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOGOCH, SAMUEL
 ; APPLICANT: BOGOCH, ELENORE S.
 ; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
 ; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
 ; FILE REFERENCE: 09425-46904
 ; CURRENT APPLICATION NUMBER: US/10/105,232
 ; CURRENT FILING DATE: 2002-03-26
 ; PRIOR APPLICATION NUMBER: 60/303,396
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: 60/278,761
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: 09/146,755
 ; PRIOR FILING DATE: 1998-09-04
 ; PRIOR APPLICATION NUMBER: 09/817,144
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: 08/198,139
 ; PRIOR FILING DATE: 1994-02-17
 ; NUMBER OF SEQ ID NOS: 535
 ; SOFTWARE: Patentin 2.1
 ; SEQ ID NO 303
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Plasmodium falciparum
 US-10-105-232-303

Query Match 4.3%; Score 6; DB 12; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSQ 136
 Db 15 SLKSQ 20

RESULT 36
 US-10-189-437-290
 ; Sequence 290, Application US/10189437
 ; Publication No. US20030194414A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOGOCH, SAMUEL
 ; APPLICANT: BOGOCH, ELENORE S.
 ; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
 ; FILE REFERENCE: 09425/46905
 ; CURRENT APPLICATION NUMBER: US/10/189,437
 ; CURRENT FILING DATE: 2002-07-08
 ; PRIOR APPLICATION NUMBER: 10/105,232
 ; PRIOR FILING DATE: 2002-03-26
 ; PRIOR APPLICATION NUMBER: 09/984,057
 ; PRIOR FILING DATE: 2001-10-26
 ; PRIOR APPLICATION NUMBER: 60/303,396
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: 60/278,761

; PRIOR FILING DATE: 2001-03-27
 ; NUMBER OF SEQ ID NOS: 729
 ; SOFTWARE: Patentin 2.1
 ; SEQ ID NO 290
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Plasmodium falciparum
 US-10-189-437-290

Query Match 4.3%; Score 6; DB 12; Length 21;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSQ 136
 Db 15 SLKSQ 20

RESULT 37
 US-10-105-232-302
 ; Sequence 302, Application US/10105232
 ; Publication No. US20030180328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOGOCH, SAMUEL
 ; APPLICANT: BOGOCH, ELENORE S.
 ; TITLE OF INVENTION: REPLIKIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
 ; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
 ; FILE REFERENCE: 09425-46904
 ; CURRENT APPLICATION NUMBER: US/10/105,232
 ; CURRENT FILING DATE: 2002-03-26
 ; PRIOR APPLICATION NUMBER: 60/303,396
 ; PRIOR FILING DATE: 2001-07-09
 ; PRIOR APPLICATION NUMBER: 60/278,761
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: 09/146,755
 ; PRIOR FILING DATE: 1998-09-04
 ; PRIOR APPLICATION NUMBER: 09/817,144
 ; PRIOR FILING DATE: 2001-03-27
 ; PRIOR APPLICATION NUMBER: 08/198,139
 ; PRIOR FILING DATE: 1994-02-17
 ; NUMBER OF SEQ ID NOS: 535
 ; SOFTWARE: Patentin 2.1
 ; SEQ ID NO 302
 ; LENGTH: 22
 ; TYPE: PRT
 ; ORGANISM: Plasmodium falciparum
 US-10-105-232-302

Query Match 4.3%; Score 6; DB 12; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSQ 136
 Db 15 SLKSQ 20

RESULT 38
 US-10-189-437-289
 ; Sequence 289, Application US/10189437
 ; Publication No. US20030194414A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOGOCH, SAMUEL
 ; APPLICANT: BOGOCH, ELENORE S.
 ; TITLE OF INVENTION: REPLIKIN PEPTIDES AND ANTIBODIES THEREFORE
 ; FILE REFERENCE: 09425/46905
 ; CURRENT APPLICATION NUMBER: US/10/189,437
 ; CURRENT FILING DATE: 2002-07-08
 ; PRIOR APPLICATION NUMBER: 10/105,232
 ; PRIOR FILING DATE: 2002-03-26
 ; PRIOR APPLICATION NUMBER: 09/984,057
 ; PRIOR FILING DATE: 2001-10-26
 ; PRIOR APPLICATION NUMBER: 60/303,396

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; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 289
; LENGTH: 22
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-189-437-289

Query Match          4.3%; Score 6; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSOG 136
Db 15 SLKSOG 20

RESULT 39
US-09-864-761-47718
; Sequence 47718, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47718

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; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006230.11
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 12
US-09-864-761-47718

Query Match          4.3%; Score 6; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 RVLPGT 56
Db 12 RVLPGT 17

RESULT 40
US-10-105-232-301
; Sequence 301, Application US/10105232
; Publication No. US20030180328A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS
; FILE REFERENCE: 09425-46904
; CURRENT APPLICATION NUMBER: US/10/105,232
; CURRENT FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 301
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-105-232-301

Query Match          4.3%; Score 6; DB 12; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 131 SLKSOG 136
Db 15 SLKSOG 20

Search completed: November 14, 2003, 10:57:33
Job time : 32 secs

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M protein - protein search, using sw model

un on: November 14, 2003, 10:48:51 ; Search time 20 Seconds
(without alignments)
677.989 Million cell updates/sec

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effect score: 141
sequence: 1 MESTSTTNFVAENRPTGE.....RAEYFRHLRSKQGVNRLI 141

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searched: 283308 seqs, 96168682 residues

ord size : 0

total number of hits satisfying chosen parameters: 283308

inimum DB seq length: 0
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ost-processing: Listing first 1000 summaries

atabase :

- PIR 76:*
- 1: p1r1:*
- 2: p1r2:*
- 3: p1r3:*
- 4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
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2	8	5.7	559	G84642	hypothetical prote
3	8	5.7	707	T14195	extensin homolog T
4	7	5.0	105	S72893	hypothetical prote
5	7	5.0	148	S73004	hypothetical prote
6	7	5.0	154	A46669	mitochondrial rece
7	7	5.0	215	B57055	melanocortin-4 rec
8	7	5.0	237	AE3619	transcription regu
9	7	5.0	238	H71291	probable flagellar
10	7	5.0	289	D70748	probable formamido
11	7	5.0	323	AH0552	protein-export mem
12	7	5.0	330	G83517	probable glycosyl
13	7	5.0	332	AS7055	melanocortin recep
14	7	5.0	332	G90291	endoglucanase prec
15	7	5.0	338	B83303	phenylalanyl-tRNA
16	7	5.0	339	T34158	hypothetical prote
17	7	5.0	350	S22366	phenylalanine-tRNA
18	7	5.0	362	S45887	ribosomal protein
19	7	5.0	362	S50993	ribosomal protein
20	7	5.0	363	1 BVBK2	MAK32 protein - ye
21	7	5.0	378	AD1188	membrane proteins
22	7	5.0	378	AD1546	membrane protein h
23	7	5.0	409	A70647	probable PPE prote
24	7	5.0	409	A70932	probable PPE prote
25	7	5.0	424	1 ZZRCL	modulation protein
26	7	5.0	468	F87108	probable amidase
27	7	5.0	473	T28052	hypothetical prote
28	7	5.0	491	F83383	probable flavin-bi
29	7	5.0	506	C70468	phosphoribosylamin

30	7	5.0	524	2 D70861	probable monoxigen
31	7	5.0	527	2 A83453	probable flavin-co
32	7	5.0	538	1 T40151	histidine-tRNA lig
33	7	5.0	701	1 S46458	transcription fact
34	7	5.0	702	1 G01840	t-box protein 2 -
35	7	5.0	731	2 AH2546	hypothetical prote
36	7	5.0	748	2 F91089	PTS system transcr
37	7	5.0	748	2 H85934	phosphotransferase
38	7	5.0	748	2 F65065	hypothetical prote
39	7	5.0	753	2 T32844	hypothetical prote
40	7	5.0	770	2 S59623	tropoelastin - she
41	7	5.0	841	2 T01046	hypothetical prote
42	7	5.0	860	1 EAMS	elastin precursor
43	7	5.0	864	1 EART	glycine dehydrogen
44	7	5.0	1057	2 A42109	probable pyruvate
45	7	5.0	1184	2 G71262	RAD9 protein - yea
46	7	5.0	1309	1 BVBK2	hypothetical prote
47	7	5.0	1447	2 T15200	hypothetical prote
48	7	5.0	4385	2 T29042	subtilisin inhibit
49	6	4.3	34	2 FC1272	alkaline proteinas
50	6	4.3	34	2 PC1261	hypothetical prote
51	6	4.3	44	2 A84184	H+-transporting tw
52	6	4.3	54	2 S70600	unknown protein en
53	6	4.3	62	2 F85709	hypothetical prote
54	6	4.3	67	2 A81189	hypothetical prote
55	6	4.3	70	2 T02541	hypothetical prote
56	6	4.3	74	2 A87956	hypothetical prote
57	6	4.3	75	2 AG1731	hypothetical prote
58	6	4.3	77	2 T20897	hypothetical prote
59	6	4.3	78	2 A75411	hypothetical prote
60	6	4.3	86	2 A87515	hypothetical prote
61	6	4.3	89	2 C82331	hypothetical prote
62	6	4.3	96	4 Q0EC31	hypothetical prote
63	6	4.3	99	2 A97413	hypothetical prote
64	6	4.3	101	2 C72486	conserved hypothe
65	6	4.3	102	2 A12630	oxy upstream of m
66	6	4.3	102	2 B48360	hypothetical prote
67	6	4.3	103	2 E75071	hypothetical prote
68	6	4.3	104	2 F72369	conserved hypothe
69	6	4.3	104	2 G68939	probable arsenate
70	6	4.3	106	2 JQ0234	hypothetical 12.5K
71	6	4.3	107	2 JX0361	subtilisin-trypsin
72	6	4.3	111	2 T17582	hypothetical prote
73	6	4.3	111	2 S14855	hypothetical prote
74	6	4.3	116	2 G82048	probable 5-carboxy
75	6	4.3	116	2 G72520	hypothetical prote
76	6	4.3	121	2 F84868	hypothetical prote
77	6	4.3	122	2 AG0221	conserved hypothe
78	6	4.3	123	2 F82835	6-pyruvoyl tetrahy
79	6	4.3	124	2 S23652	hypothetical prote
80	6	4.3	126	2 S41186	gene 39 protein -
81	6	4.3	128	2 T13630	hypothetical prote
82	6	4.3	128	2 T13325	hypothetical prote
83	6	4.3	128	2 E70547	hypothetical prote
84	6	4.3	131	2 B84163	hypothetical prote
85	6	4.3	132	2 E72727	probable ribosomal
86	6	4.3	135	2 H87410	hypothetical prote
87	6	4.3	137	2 H87270	hypothetical prote
88	6	4.3	138	2 T49392	related to pullula
89	6	4.3	141	2 T08790	hypothetical prote
90	6	4.3	143	2 E87574	Rif2 family protei
91	6	4.3	144	2 S01290	apolipoprotein B -
92	6	4.3	144	2 AG3178	transcription regu
93	6	4.3	145	2 B86751	prophage pi2 prote
94	6	4.3	145	2 T08435	la costa protein -
95	6	4.3	148	2 T48981	hypothetical prote
96	6	4.3	148	2 AE1811	hypothetical prote
97	6	4.3	149	1 VHBPF6	major nucleocapsid
98	6	4.3	150	2 S33784	hemoglobin VII - m
99	6	4.3	154	2 A82096	xanthine-guanine p
100	6	4.3	154	2 T34641	probable integral
101	6	4.3	157	2 S35037	helix-loop-helix p
102	6	4.3	158	2 F95051	acetolactate synth

103	6	4.3	158	2	D83382	hypothetical prote	176	232	2	S18139	dehydrin DHN3 - ga
104	6	4.3	159	2	E89861	Na+/H+ antiporter	177	232	2	B96803	hypothetical prote
105	6	4.3	160	2	C72318	hypothetical prote	178	232	2	A13559	endopeptidase Ia (
106	6	4.3	161	2	T21995	hypothetical prote	179	233	2	C90507	hypothetical prote
107	6	4.3	162	2	B71085	hypothetical prote	180	233	2	S44882	2C262.2 protein -
108	6	4.3	164	2	E75100	hypothetical prote	181	234	2	D48364	hypothetical prote
109	6	4.3	165	2	T35813	hypothetical prote	182	235	2	PC2022	cytochrome-c oxida
110	6	4.3	166	2	D75292	conserved hypothet	183	235	2	D48364	mucin like protein
111	6	4.3	167	2	B97922	acetolactate synth	184	235	2	C64915	dethiobiotin synth
112	6	4.3	168	2	JC5165	acetolactate synth	185	235	2	C90916	dethiobiotin synth
113	6	4.3	169	2	E70855	probable ilvN prot	186	235	2	H85764	lipocate-protein li
114	6	4.3	170	2	T45414	hypothetical prote	187	235	2	G86567	hypothetical prote
115	6	4.3	171	2	G87656	conserved hypothet	188	235	2	F70405	lipocate-protein li
116	6	4.3	172	2	D87299	acetyltransferase,	189	235	2	F72056	conserved hypothet
117	6	4.3	173	2	B64094	ribosomal protein	190	236	2	B69090	conserved hypothet
118	6	4.3	174	2	C70844	probable moaC3 pro	191	236	2	A12432	hypothetical prote
119	6	4.3	175	2	S76780	hypothetical prote	192	237	2	A75400	probable phosphogl
120	6	4.3	176	2	T08444	hypothetical prote	193	237	2	T76765	hypothetical prote
121	6	4.3	177	2	E69193	conserved hypothet	194	237	2	F97416	hypothetical prote
122	6	4.3	178	2	TPCHIS	troponin I, fast s	195	239	2	JC7768	blue fluorescent p
123	6	4.3	179	2	B83310	single-strand DNA	196	239	2	H75293	probable manganese
124	6	4.3	180	2	A23569	troponin I, fast s	197	240	2	F90885	hypothetical prote
125	6	4.3	181	2	G83379	probable fibrial	198	240	2	C90293	hypothetical prote
126	6	4.3	182	1	TPRBIW	troponin I, slow s	199	240	2	A85733	hypothetical prote
127	6	4.3	183	1	TPHUIW	troponin I, slow s	200	240	2	B64897	hypothetical prote
128	6	4.3	184	2	B44786	troponin I, slow s	201	241	2	SI9999	hypothetical prote
129	6	4.3	185	2	B85680	unknown protein en	202	241	2	F87189	conserved hypothet
130	6	4.3	186	2	A71286	conserved hypothet	203	242	2	I62393	outer membrane pro
131	6	4.3	187	2	T06769	probable glycogen(204	244	2	B72099	conserved hypothet
132	6	4.3	188	2	E64942	hypothetical 21.4	205	244	2	B86523	pp-loop type ATPas
133	6	4.3	189	2	D69336	guanylate kinase (206	245	2	T50626	hypothetical prote
134	6	4.3	190	2	D69013	conserved hypothet	207	245	2	AB0589	hypothetical prote
135	6	4.3	191	2	S22636	hypothetical prote	208	245	2	JC6191	ATP-binding casset
136	6	4.3	192	2	T06813	dehydrin 3 - Garde	209	249	2	T48684	hypothetical prote
137	6	4.3	193	2	F83241	outer membrane lip	210	250	2	T12864	ribosomal protein
138	6	4.3	194	2	E84309	hypothetical prote	211	251	2	S40735	LSU ribosomal prot
139	6	4.3	195	2	A69429	hypothetical prote	212	251	2	B64322	hypothetical prote
140	6	4.3	196	2	T42969	hypothetical prote	213	252	2	C69490	transcription regu
141	6	4.3	201	2	T43480	hypothetical prote	214	252	2	T09560	leu ribosomal prot
142	6	4.3	202	2	B83606	hypothetical prote	215	252	2	H72469	hypothetical prote
143	6	4.3	203	2	AD2405	hypothetical prote	216	252	2	AC1338	probable ribosomal
144	6	4.3	204	2	S52644	phycobilisome matu	217	253	2	A11708	hypothetical prote
145	6	4.3	205	2	E83515	conserved hypothet	218	253	2	T49820	transcription regu
146	6	4.3	206	2	T46194	hypothetical prote	219	253	2	H75147	hypothetical prote
147	6	4.3	207	2	G81336	hypothetical prote	220	255	2	G71187	leu ribosomal prot
148	6	4.3	208	2	S51098	uracil phosphoribo	221	255	2	T09558	probable ribosomal
149	6	4.3	209	2	E90004	probable alkyl hyd	222	255	2	C88956	hypothetical prote
150	6	4.3	210	2	C82748	uracil phosphoribo	223	255	2	I40170	protein K04F1.5 [l
151	6	4.3	211	2	F71111	stringent starvati	224	258	2	S25271	hypothetical prote
152	6	4.3	212	2	S77269	hypothetical prote	225	258	2	D84078	gene Cpl2 protein
153	6	4.3	213	2	A95863	hypothetical prote	226	259	2	D47031	p-nitrophenyl phos
154	6	4.3	214	2	H82314	hypothetical prote	227	260	1	T45251	orf2 3', of bah - S
155	6	4.3	215	2	T36491	conserved hypothet	228	261	2	T45251	probable cyclase h
156	6	4.3	216	2	S01358	probable gntR-fam	229	262	2	T17442	ybtT protein - Yer
157	6	4.3	217	2	T15053	salivary glue prot	230	265	1	G69084	conserved hypothet
158	6	4.3	218	2	A71711	ribonuclease (EC 3	231	265	2	T42419	hypothetical prote
159	6	4.3	219	2	A83257	hypothetical prote	232	265	2	T40259	hypothetical prote
160	6	4.3	220	2	AG0670	probable regulator	233	265	2	T40868	hypothetical prote
161	6	4.3	221	2	B69079	alkyl hydroperoxid	234	267	2	T47050	hypothetical prote
162	6	4.3	222	2	F72108	amino acid ABC tra	235	267	2	T30342	ilp4 protein - Yer
163	6	4.3	223	2	G86514	ABC amino acid tra	236	267	2	AH0232	versiniaabactin bio
164	6	4.3	224	2	G86514	hypothetical prote	237	267	2	AI3010	hypothetical prote
165	6	4.3	225	2	E64830	cytidylate kinase	238	267	2	B98273	iron(III) diclrat
166	6	4.3	226	2	E64830	cytidylate kinase	239	269	2	A95906	hypothetical prote
167	6	4.3	227	2	A95753	cytidylate kinase	240	271	2	T51249	yjcl protein [impo
168	6	4.3	228	2	G85616	cytidylate kinase	241	274	2	I46929	stem cell factor -
169	6	4.3	229	2	AB0614	cytidylate kinase	242	275	2	B81099	formamidopyrimidin
170	6	4.3	230	2	T34197	GntR family transc	243	275	2	B81842	DNA-formamidopyrim
171	6	4.3	231	2	T834197	hypothetical prote	244	275	2	S44961	lmbN protein - Str
172	6	4.3	232	2	B89923	hypothetical prote	245	275	2	AC1772	conserved hypothet
173	6	4.3	233	2	B82691	N-(5', phosphoribos	246	276	2	T49220	conserved hypothet
174	6	4.3	234	2	C82141	cytidylate kinase	247	276	2	D70191	casein kinase II (
175	6	4.3	235	2	A10169	cytidylate kinase	248	279	2	S67132	hypothetical prote

249	6	4.3	280	2	G9508	protein F27F5.5 [i	322	6	4.3	331	2	D72314	ribose ABC transpo
250	6	4.3	281	2	T45926	hypothetical prote	323	6	4.3	332	2	T35917	probable regulator
251	6	4.3	281	2	E75195	hypothetical prote	324	6	4.3	332	2	T51269	hypothetical prote
252	6	4.3	281	2	H71227	hypothetical prote	325	6	4.3	333	2	AH2179	DnaJ protein [impo
253	6	4.3	281	2	AF0505	probable exported	326	6	4.3	333	2	AI0940	probable ABC trans
254	6	4.3	282	2	D87341	forminosyltransferase	327	6	4.3	333	2	TO1846	hypothetical prote
255	6	4.3	282	2	E71444	homeobox protein H	328	6	4.3	336	2	G95003	membrane protein [
256	6	4.3	282	2	F64695	biotin synthetase	329	6	4.3	336	2	AS4035	lipoate-protein li
257	6	4.3	282	2	H71822	UTP-glucose-1-phos	330	6	4.3	338	1	TVMSF5	transforming prote
258	6	4.3	283	2	S63639	hypothetical prote	331	6	4.3	338	2	H87510	phenylalanine-tRNA
259	6	4.3	285	2	D69184	hypothetical prote	332	6	4.3	338	2	D70382	polyprenyl synthet
260	6	4.3	285	2	C95327	hypothetical prote	333	6	4.3	338	2	DS9102	protein F2585.2 [i
261	6	4.3	286	2	AH1038	site-specific DNA-	334	6	4.3	338	2	S72441	MG032 homolog Bol
262	6	4.3	287	2	AB2354	dihydropterate sy	335	6	4.3	339	2	S86614	phenylalanyl tRNA
263	6	4.3	287	2	F82265	conserved hypotet	336	6	4.3	339	2	B72011	phenylalanine-tRNA
264	6	4.3	287	2	S28371	viomycin kinase [E	337	6	4.3	339	2	AD3501	Mg(2+) chelataase f
265	6	4.3	287	2	S74050	hypothetical prote	338	6	4.3	340	2	S74768	UDPglucose 4-epime
266	6	4.3	287	2	A12609	regulator protein	339	6	4.3	340	2	B97876	conserved hypotet
267	6	4.3	288	2	H97391	H+-transporting tw	340	6	4.3	341	2	T41286	malate dehydrogena
268	6	4.3	288	2	S73016	probable regulator	341	6	4.3	341	2	F81727	phenylalanyl-tRNA
269	6	4.3	288	2	E86717	hypothetical prote	342	6	4.3	341	2	D64221	phenylalanine-tRNA
270	6	4.3	288	2	T47614	hypothetical prote	343	6	4.3	341	2	E96019	probable sugar upt
271	6	4.3	289	2	E70984	probable drB prot	344	6	4.3	341	2	D64159	hypothetical prote
272	6	4.3	289	2	A87534	carboxylesterase f	345	6	4.3	341	2	T47653	pectate lyase-like
273	6	4.3	289	2	F97322	uncharacterized co	346	6	4.3	342	2	D71465	phenylalanine-tRNA
274	6	4.3	291	2	C87700	UTP-glucose-1-phos	347	6	4.3	342	2	T29245	hypothetical prote
275	6	4.3	292	2	T06201	xyloglucan endo-1,	348	6	4.3	342	2	S09786	hypothetical prote
276	6	4.3	292	2	E71885	hypothetical prote	349	6	4.3	343	2	A45073	hypothetical prote
277	6	4.3	292	2	A47125	transcription acti	350	6	4.3	343	2	H96654	Gal beta 1,3GalNAC
278	6	4.3	293	1	WMBP11	gene 11 protein -	351	6	4.3	343	2	G81934	FlaPI7.15 [importe
279	6	4.3	293	1	WMBPL9	gene 11 protein -	352	6	4.3	344	2	H81171	probable dihydroor
280	6	4.3	293	2	T06232	Ps16 protein - whe	353	6	4.3	344	2	T24053	dihydroorotase NMB
281	6	4.3	294	2	E82723	hypothetical prote	354	6	4.3	345	2	T14707	hypothetical prote
282	6	4.3	294	2	T05725	cp31AHV protein -	355	6	4.3	345	2	T17608	DNA ligase homolog
283	6	4.3	295	2	A12683	transcription regu	356	6	4.3	346	2	A99173	probable GDPmannos
284	6	4.3	297	2	H72076	hypothetical prote	357	6	4.3	346	2	AG0302	hypothetical prote
285	6	4.3	299	2	T24768	hypothetical prote	358	6	4.3	347	2	AB0509	Laci-family transc
286	6	4.3	300	2	H87631	integral membrane	359	6	4.3	347	2	T20472	[citrate (PRO-3S) -
287	6	4.3	300	2	C84732	hypothetical prote	360	6	4.3	347	2	S69719	hypothetical prote
288	6	4.3	302	2	I39495	hypothetical prote	361	6	4.3	348	2	B95970	hypothetical prote
289	6	4.3	302	2	F95990	probable transcrip	362	6	4.3	349	2	S67858	probable glutathio
290	6	4.3	304	2	G85714	hypothetical prote	363	6	4.3	351	1	C69198	gum protein - Xan
291	6	4.3	305	1	S52775	hypothetical prote	364	6	4.3	352	2	S67935	phospho-N-acetylmu
292	6	4.3	308	2	B84311	hypothetical prote	365	6	4.3	353	2	B36963	branched-chain ket
293	6	4.3	311	2	AH2804	hypothetical prote	366	6	4.3	353	2	S29788	bcsA 5'--region pro
294	6	4.3	313	2	AD0920	conserved hypotet	367	6	4.3	353	2	S41958	glucose 1-dehydrog
295	6	4.3	313	2	H97583	porphobilinogen de	368	6	4.3	353	2	S29788	pupal cuticicle pro
296	6	4.3	316	2	G97465	hypothetical prote	369	6	4.3	355	2	T10722	anthocyanidin synt
297	6	4.3	316	2	D82857	lysR type transcri	370	6	4.3	355	2	A72279	sugar ABC transpor
298	6	4.3	317	2	B72395	hypothetical prote	371	6	4.3	357	1	Q0MSLL	retrovirus-related
299	6	4.3	319	2	E96715	alcohol dehydrogen	372	6	4.3	358	2	S65163	hypothetical prote
300	6	4.3	321	2	B64797	protein FAN2.12 [i	373	6	4.3	359	2	T42087	probable 6-phospho
301	6	4.3	321	2	B87712	lipoic acid synthet	374	6	4.3	361	2	T17282	hypothetical prote
302	6	4.3	321	2	F85562	lipoate synthesis,	375	6	4.3	361	2	IS0475	hypothetical prote
303	6	4.3	321	2	T06845	hypothetical prote	376	6	4.3	364	1	S77360	dopamine D1 recept
304	6	4.3	322	2	H64933	succinylglutamate	377	6	4.3	364	1	C87125	chiD protein - Syn
305	6	4.3	322	2	S09335	hypothetical prote	378	6	4.3	365	2	T15010	hypothetical prote
306	6	4.3	322	2	F85783	hypothetical prote	379	6	4.3	365	2	E83710	hypothetical prote
307	6	4.3	322	2	T22403	hypothetical prote	380	6	4.3	367	2	T09376	hypothetical prote
308	6	4.3	323	2	G87358	dienelactone hydro	381	6	4.3	368	2	T05542	hypothetical prote
309	6	4.3	325	2	A82669	oxidative stress t	382	6	4.3	368	2	T40115	uv excision repair
310	6	4.3	325	2	S57977	CCCH zinc finger p	383	6	4.3	369	2	T06723	hypothetical prote
311	6	4.3	325	2	D90530	hypothetical prote	384	6	4.3	369	2	AC2702	outer membrane pro
312	6	4.3	327	2	C64570	phenylalanine-tRNA	385	6	4.3	369	2	C97484	outer membrane pro
313	6	4.3	328	2	E71863	phenylalanine-tRNA	386	6	4.3	369	2	H87633	threonine aldolase
314	6	4.3	328	2	T20856	hypothetical prote	387	6	4.3	370	2	B69029	pre-mRNA splicing
315	6	4.3	329	2	H83907	hypothetical prote	388	6	4.3	370	2	AD2375	hypothetical prote
316	6	4.3	329	2	C96033	cytochrome aa3 qui	389	6	4.3	370	2	H69291	conserved hypotet
317	6	4.3	329	2	AD3617	probable regulator	390	6	4.3	371	2	T15095	hypothetical prote
318	6	4.3	330	2	T02525	1-carboxy-3-chloro	391	6	4.3	371	2	T01303	hypothetical prote
319	6	4.3	330	2	T02525	probable DOF zinc	392	6	4.3	371	2	D84186	hypothetical prote
320	6	4.3	331	1	S44304	phenol 2-monooxyge	393	6	4.3	371	2	H81303	branched-chain ami
321	6	4.3	331	1	B37831	phenol 2-monooxyge	394	6	4.3	374	2	T36641	probable ABC-type

395	6	4.3	374	2	E90454	hypothetical prote	468	6	4.3	433	2	D90176	hypothetical prote
396	6	4.3	374	2	F96702	hypothetical prote	469	6	4.3	434	2	S28312	hypothetical prote
397	6	4.3	376	2	T35085	hypothetical prote	470	6	4.3	434	2	B69271	hypothetical prote
398	6	4.3	376	2	G90347	transposase ISC131	471	6	4.3	437	2	AH3285	gcpE protein [impo
399	6	4.3	377	2	F97267	uncharacterized co	472	6	4.3	437	2	H36933	aspartate kinase [
400	6	4.3	378	2	T06744	hypothetical prote	473	6	4.3	438	2	S73952	adhesin P1 precurs
401	6	4.3	380	1	W22MP	dihydrodipicolinat	474	6	4.3	438	2	S71157	cytochrome c bioge
402	6	4.3	380	2	T05220	hypothetical prote	475	6	4.3	440	2	G72317	chromosomal replic
403	6	4.3	381	2	G71130	hypothetical prote	476	6	4.3	440	2	AH1395	conserved hypothet
404	6	4.3	383	2	S53716	delta-like homeoti	477	6	4.3	440	2	AH1770	conserved hypothet
405	6	4.3	384	2	D87471	ROK family protein	478	6	4.3	441	2	H82617	folylpolyglutamate
406	6	4.3	385	2	T21756	hypothetical prote	479	6	4.3	441	2	E96584	hypothetical prote
407	6	4.3	385	2	JC7751	exo-alpha-sialidas	480	6	4.3	446	1	DXHUI1	dopamine receptor
408	6	4.3	386	2	T12048	ribosomal protein	481	6	4.3	446	2	D17217	dopamine receptor
409	6	4.3	386	2	S72168	dopamine receptor	482	6	4.3	446	2	G87448	succinylarginine d
410	6	4.3	387	2	E71711	probable o-sialogl	483	6	4.3	447	2	T13091	probable minor cap
411	6	4.3	387	2	C82336	conserved hypothet	484	6	4.3	449	2	A30303	interferon-related
412	6	4.3	387	2	H64182	xylose operon regl	485	6	4.3	449	2	A44989	interferon-related
413	6	4.3	388	2	E84025	hypothetical prote	486	6	4.3	449	2	JC7306	extracellular prot
414	6	4.3	389	2	T20216	hypothetical prote	487	6	4.3	450	2	A55886	dopamine receptor
415	6	4.3	390	2	T25642	hypothetical prote	488	6	4.3	451	2	I51659	dopamine D1A recep
416	6	4.3	391	2	H90308	transposase ISC131	489	6	4.3	451	2	F75131	hypothetical prote
417	6	4.3	393	2	D70539	probable citrate s	490	6	4.3	451	2	C75075	hypothetical prote
418	6	4.3	393	2	E90272	transposase ISC131	491	6	4.3	454	2	C82941	ATP synthase beta
419	6	4.3	393	2	AE1754	portal protein [ba	492	6	4.3	454	2	H90980	probable amino aci
420	6	4.3	394	2	T08757	probable translati	493	6	4.3	454	2	E85826	probable amino aci
421	6	4.3	394	2	S74643	proteinase hbaA (E	494	6	4.3	454	2	E64966	probable amino aci
422	6	4.3	394	2	G83027	conserved hypothet	495	6	4.3	454	2	AG0783	probable amino aci
423	6	4.3	395	2	T38885	probable cysteine	496	6	4.3	454	2	C85173	thiophene and fura
424	6	4.3	395	2	C90328	transposase ISC131	497	6	4.3	454	2	A98209	hypothetical prote
425	6	4.3	396	2	S55281	translation elonga	498	6	4.3	454	2	C86055	hypothetical prote
426	6	4.3	396	2	S27870	house-keeping prot	499	6	4.3	454	2	AE0957	thiophene and fura
427	6	4.3	397	2	A82854	flavohemoprotein X	500	6	4.3	454	2	T02680	hypothetical prote
428	6	4.3	397	2	A75137	hypothetical prote	501	6	4.3	457	2	I51660	dopamine D1B recep
429	6	4.3	399	1	S76745	hypothetical prote	502	6	4.3	458	2	A44487	probable replicati
430	6	4.3	399	2	F69034	argininosuccinate	503	6	4.3	458	2	S24457	hypothetical prote
431	6	4.3	399	2	C90455	transposase ISC131	504	6	4.3	459	2	D34791	interleukin-7 rece
432	6	4.3	400	2	S32804	beta-3-adrenergic	505	6	4.3	459	2	A56849	dopamine receptor-
433	6	4.3	401	2	F97260	uncharacterized co	506	6	4.3	459	2	A75097	hypothetical prote
434	6	4.3	402	1	E64822	probable membrane	507	6	4.3	459	2	D70717	hypothetical prote
435	6	4.3	402	2	A85595	probable DEOR-type	508	6	4.3	459	2	T31608	hypothetical prote
436	6	4.3	402	2	E90744	probable DEOR-type	509	6	4.3	460	2	H65336	hypothetical prote
437	6	4.3	402	2	T09882	probable PPE prote	510	6	4.3	461	2	T36599	probable beta-lact
438	6	4.3	403	2	B90290	transposase ISC131	511	6	4.3	462	2	C83920	dopamine receptor-
439	6	4.3	404	2	AB1336	argininosuccinate	512	6	4.3	462	2	B56849	hypothetical prote
440	6	4.3	404	2	AH1706	argininosuccinate	513	6	4.3	465	2	I51661	dopamine D1C recep
441	6	4.3	404	2	S45923	probable phosphopa	514	6	4.3	469	2	T50934	dioxynase Dita1,
442	6	4.3	404	2	S42831	F40R12.2 protein -	515	6	4.3	470	2	D27222	probable MRSA prot
443	6	4.3	406	2	T48103	mRNA binding prote	516	6	4.3	471	2	A82155	hypothetical prote
444	6	4.3	407	2	T48308	60S ribosomal prot	517	6	4.3	471	2	S35635	DNA injection prot
445	6	4.3	408	2	C66903	hypothetical prote	518	6	4.3	472	2	AG3600	cellulose synthase
446	6	4.3	408	2	B90326	transposase ISC131	519	6	4.3	472	2	D81782	oxygen-independent
447	6	4.3	410	1	S68153	cellulase (EC 3.2.	520	6	4.3	473	2	H81204	oxygen-independent
448	6	4.3	411	2	C90458	transposase ISC131	521	6	4.3	474	2	T31770	hypothetical prote
449	6	4.3	411	2	AG3003	conserved hypothet	522	6	4.3	474	2	T10271	capsid-associated
450	6	4.3	411	2	B98280	hypothetical prote	523	6	4.3	475	2	T27811	hypothetical prote
451	6	4.3	413	1	S34305	modulation protein	524	6	4.3	476	2	A70704	probable rocE prot
452	6	4.3	413	1	S28602	translation releas	525	6	4.3	480	2	G84360	phenylalanine-tRNA
453	6	4.3	414	2	D68547	protein F02A9.4b [526	6	4.3	481	2	T03660	phosphoglycerate k
454	6	4.3	416	2	F71379	heat shock protein	527	6	4.3	481	2	S74934	pleD-1 protein - S
455	6	4.3	416	2	S76310	hypothetical prote	528	6	4.3	485	2	B88114	protein F53C3.9 [i
456	6	4.3	417	2	S57820	pyruvate decarboxy	529	6	4.3	485	2	C75460	hypothetical prote
457	6	4.3	417	2	T24618	hypothetical prote	530	6	4.3	486	2	I39523	dehydroshikimate d
458	6	4.3	421	2	T41577	pombe specific con.	531	6	4.3	486	2	T38174	probable CCS1/Glo3
459	6	4.3	423	2	T50923	acetylmorphine tr	532	6	4.3	487	1	DXRTD1	dopamine receptor
460	6	4.3	423	2	AI3309	tRNA adenylyltrans	533	6	4.3	488	2	T41160	hypothetical prote
461	6	4.3	424	2	G83733	hypothetical prote	534	6	4.3	490	2	F38462	S-mephenytoin 4'-h
462	6	4.3	425	2	T16433	hypothetical prote	535	6	4.3	490	2	T06714	probable cytochrom
463	6	4.3	426	2	I48379	gene hb protein -	536	6	4.3	490	2	G85354	hypothetical prote
464	6	4.3	426	2	A12498	L-amino acid oxida	537	6	4.3	490	2	E71486	probable s/t prote
465	6	4.3	428	2	S73379	adhesin P1 precurs	538	6	4.3	491	2	F70538	probable ppk prot
466	6	4.3	432	2	B84127	hypothetical prote	539	6	4.3	491	1	FGHUB	fibrinogen beta ch
467	6	4.3	433	1	E64242	GTP-binding protei	540	6	4.3	491	2	C83206	probable outer mem

541	6	4.3	492	2	D70649	cytochrome P450 Rv	614	6	4.3	578	2	H75256	malate oxidoreduct
542	6	4.3	492	2	G70899	probable monooxyge	615	6	4.3	581	2	A49073	HSN motor neurons
543	6	4.3	492	2	T32685	hypothetical prote	616	6	4.3	581	2	C86430	hypothetical prote
544	6	4.3	495	2	S43294	bone morphogenetic	617	6	4.3	599	2	JG0196	protein kinase DYR
545	6	4.3	495	2	S75340	NADH2 dehydrogenas	618	6	4.3	590	2	S16411	terminase ATPase c
546	6	4.3	496	2	E90181	hypothetical prote	619	6	4.3	591	2	F95084	pyruvate oxidase (
547	6	4.3	497	2	T27012	hypothetical prote	620	6	4.3	591	2	B97952	pyruvate oxidase (
548	6	4.3	498	2	T40776	MSF membrane trans	621	6	4.3	592	2	D70863	hypothetical prote
549	6	4.3	499	1	C44767	benzoylformate dec	622	6	4.3	592	2	T34446	pyruvate, phosphat
550	6	4.3	499	2	T47722	probable protein k	623	6	4.3	601	2	E87028	hypothetical prote
551	6	4.3	500	1	E9FF	zip protein precur	624	6	4.3	601	2	A88923	protein W03F9.10 (
552	6	4.3	500	2	J67668	dipeptidyl-peptida	625	6	4.3	602	2	E90302	hypothetical prote
553	6	4.3	500	2	J67668	hypothetical prote	626	6	4.3	602	2	E90302	hypothetical prote
554	6	4.3	501	2	A55452	cartilage-derived	627	6	4.3	604	1	JP0001	glucan 1,4-alpha-g
555	6	4.3	501	2	JC2347	growth/differentia	628	6	4.3	605	2	S42639	hypothetical prote
556	6	4.3	504	2	T04810	aspartate-tRNA lig	629	6	4.3	607	1	A96693	Arr-dependent RNA
557	6	4.3	504	2	B70821	hypothetical prote	630	6	4.3	609	2	T15059	probable receptor
558	6	4.3	506	2	AB3411	cysteine-tRNA liga	631	6	4.3	611	2	S43427	hypothetical prote
559	6	4.3	507	2	AG3187	aldenhyde dehydrog	632	6	4.3	614	2	B69332	intermediate filam
560	6	4.3	508	2	B30310	glucose transport	633	6	4.3	614	2	B69332	conserved hypothet
561	6	4.3	509	1	TVHAST	protein-tyrosine k	634	6	4.3	615	2	A83188	hypothetical prote
562	6	4.3	509	2	A32101	glucose transport	635	6	4.3	616	2	H90764	hypothetical prote
563	6	4.3	509	2	A33801	muscle-fat glucose	636	6	4.3	616	2	P90911	hypothetical prote
564	6	4.3	509	2	S74935	hypothetical prote	637	6	4.3	617	2	F85627	proline-tRNA ligas
565	6	4.3	510	2	H81369	purH bifunctional	638	6	4.3	617	2	F71359	hypothetical prote
566	6	4.3	511	2	G95394	probable oxygenase	639	6	4.3	617	2	E90851	hypothetical prote
567	6	4.3	511	2	T87777	6-HYDROXY-D-NICOTI	640	6	4.3	617	2	A90874	hypothetical prote
568	6	4.3	511	2	T23354	hypothetical prote	641	6	4.3	617	2	B91066	hypothetical prote
569	6	4.3	512	2	S61905	threonine synthase	642	6	4.3	617	2	B85679	unknown protein en
570	6	4.3	514	1	QJNWPB	photosystem II chl	643	6	4.3	618	2	H85819	arsenite transport
571	6	4.3	515	2	H84013	hypothetical prote	644	6	4.3	620	2	AH1827	alpha-amyase (imp
572	6	4.3	516	2	T40631	probable membrane	645	6	4.3	620	2	B96933	amino acid transpo
573	6	4.3	516	2	F96549	hypothetical prote	646	6	4.3	621	2	T20307	hypothetical prote
574	6	4.3	516	2	F83894	hypothetical prote	647	6	4.3	624	2	D64449	threonine-tRNA lig
575	6	4.3	516	2	G95406	probable ABC trans	648	6	4.3	629	2	A69814	ABC transporter (A
576	6	4.3	517	2	H87022	hypothetical prote	649	6	4.3	629	2	JG0195	protein kinase DYR
577	6	4.3	519	2	T45447	probable two-compo	650	6	4.3	630	2	C39930	hypothetical prote
578	6	4.3	519	2	T23739	hypothetical prote	651	6	4.3	630	2	T38637	hypothetical prote
579	6	4.3	523	2	S42727	translation initia	652	6	4.3	630	2	A39344	tumor-associated m
580	6	4.3	524	2	T71961	translation initia	653	6	4.3	630	2	AC1129	Internalin B (impo
581	6	4.3	524	2	F87664	glycine cleavage s	654	6	4.3	631	2	T52257	episialin - mouse
582	6	4.3	524	2	JC7090	germ cell-less pro	655	6	4.3	632	2	G69306	NADH oxidase (noxB
583	6	4.3	525	2	A36130	transcription init	656	6	4.3	632	2	E69407	NADH oxidase (noxB
584	6	4.3	526	2	T33779	hypothetical prote	657	6	4.3	632	2	B69310	mRNA 3'-end proces
585	6	4.3	528	2	T00951	probable 3-oxoacyl	658	6	4.3	633	2	H96748	unknown protein T1
586	6	4.3	532	2	S66087	amino acid transpo	659	6	4.3	633	2	T24898	hypothetical prote
587	6	4.3	532	2	T18571	probable cycloprop	660	6	4.3	634	2	T18711	hypothetical prote
588	6	4.3	532	2	H72730	probable acyl-CoA	661	6	4.3	634	2	T18702	hypothetical prote
589	6	4.3	534	2	C70548	probable regulator	662	6	4.3	635	2	T34186	hypothetical prote
590	6	4.3	537	2	AB2766	sulfate permease (663	6	4.3	638	2	T43018	sna41 protein - fi
591	6	4.3	537	2	F97546	hypothetical prote	664	6	4.3	642	2	F72528	probable Glu-tRNA
592	6	4.3	539	2	T50579	probable membrane	665	6	4.3	645	2	H89951	threonyl-tRNA synt
593	6	4.3	540	2	A95264	probable ABC trans	666	6	4.3	645	2	G01205	TYL protein - huma
594	6	4.3	542	2	T20457	hypothetical prote	667	6	4.3	652	2	T39722	serine/threonine p
595	6	4.3	543	2	E88280	protein egl-43 (im	668	6	4.3	652	2	A69656	methyl-accepting c
596	6	4.3	544	2	A55146	guanine nucleotide	669	6	4.3	654	2	B70766	hypothetical prote
597	6	4.3	545	2	T52068	RAN GTPase-activat	670	6	4.3	656	2	D75450	extracellular solu
598	6	4.3	547	2	AC2541	hypothetical prote	671	6	4.3	659	2	S77658	hypothetical prote
599	6	4.3	554	2	E72362	dihydroxy-acid deh	672	6	4.3	659	2	T40781	26S proteinase sub
600	6	4.3	556	2	T28960	hypothetical prote	673	6	4.3	660	2	F70751	hypothetical prote
601	6	4.3	556	2	T40077	hypothetical prote	674	6	4.3	661	2	H75295	transketolase - De
602	6	4.3	557	2	AC2137	ABC transporter AT	675	6	4.3	666	2	H75295	hypothetical prote
603	6	4.3	557	2	A94297	probable lipote-p	676	6	4.3	672	2	T20310	hypothetical prote
604	6	4.3	562	2	C86138	probable lipote-p	677	6	4.3	674	2	T23235	hypothetical prote
605	6	4.3	563	2	B82579	peptide synthase X	678	6	4.3	677	2	T19281	hypothetical prote
606	6	4.3	567	2	S63778	adhesin AP65-1 pre	679	6	4.3	680	2	A42298	thimet oligopeptid
607	6	4.3	567	2	AC0143	choline dehydrogen	680	6	4.3	680	2	S47718	oligopeptidase A (
608	6	4.3	567	2	T28797	hypothetical prote	681	6	4.3	680	2	B66021	oligopeptidase A (
609	6	4.3	569	2	D96954	hypothetical prote	682	6	4.3	680	2	B91175	oligopeptidase A (
610	6	4.3	570	2	G72595	methyl-accepting c	683	6	4.3	680	2	AB0988	oligopeptidase A (
611	6	4.3	571	2	C75530	conserved hypothet	684	6	4.3	680	2	T41670	hypothetical zinc
612	6	4.3	576	2	T22700	hypothetical prote	685	6	4.3	683	2	A39784	phycobilisome anch
613	6	4.3	577	2	T40297	membrane transport	686	6	4.3	685	2	AH3414	soluble lytic mure
										691	2	T32748	hypothetical prote

587	6	4.3	692	2	C87644	fatty oxidation co	760	6	4.3	857	2	T14471	probable S-recepto
588	6	4.3	692	2	D86547	hypothetical prote	761	6	4.3	858	1	VCLJG2	env polyprotein pr
589	6	4.3	692	2	A81593	hypothetical prote	762	6	4.3	861	2	T00434	probable kinesin h
590	6	4.3	693	2	T39154	probable ABC trans	763	6	4.3	869	2	H89775	alcohol-acetaldehy
591	6	4.3	694	2	A95866	probable transketo	764	6	4.3	876	2	B96693	probable receptor
592	6	4.3	695	2	B84495	hypothetical prote	765	6	4.3	878	2	AE0478	phosphoenolpyruvat
593	6	4.3	697	2	D84429	hypothetical prote	766	6	4.3	880	2	A55201	meiosis-specific p
594	6	4.3	697	2	D83677	hypothetical prote	767	6	4.3	880	2	T42600	DNA helicase/prima
595	6	4.3	705	2	D84680	probable ABC trans	768	6	4.3	881	1	WZB8E9	99.5K DNA helicase
596	6	4.3	705	2	T34531	hypothetical prote	769	6	4.3	893	2	H95953	probable bifunctio
597	6	4.3	708	2	T19474	hypothetical prote	770	6	4.3	897	2	T06540	polyribonucleotide
598	6	4.3	708	2	T29669	hypothetical prote	771	6	4.3	900	2	A95340	cation transport p
599	6	4.3	710	2	T00055	hypothetical prote	772	6	4.3	902	2	T49878	respiratory burst
600	6	4.3	713	2	A12514	ABC transporter At	773	6	4.3	905	2	T00475	probable disease r
701	6	4.3	723	2	S51788	malate synthase (E	774	6	4.3	905	2	T23510	hypothetical prote
702	6	4.3	724	2	H87423	cation-transportin	775	6	4.3	905	2	T23229	hypothetical prote
703	6	4.3	724	2	C28332	DNA ligase Adu2082	776	6	4.3	907	2	A45560	sporozoite surface
704	6	4.3	724	2	G97609	DNA ligase (polyde	777	6	4.3	910	2	D75524	alpha-dextran endo
705	6	4.3	727	2	T29612	hypothetical prote	778	6	4.3	914	2	T25220	hypothetical prote
706	6	4.3	730	2	T05345	hypothetical prote	779	6	4.3	916	2	G82993	probable ATP-bind
707	6	4.3	731	2	T04629	hypothetical prote	780	6	4.3	921	2	F84593	hypothetical prote
708	6	4.3	733	2	AD2444	hypothetical prote	781	6	4.3	926	2	T39082	hypothetical prote
709	6	4.3	736	2	B82944	ribose/galactose A	782	6	4.3	932	2	T48761	hypothetical prote
710	6	4.3	741	2	D28572	bsg25D protein f	783	6	4.3	936	2	T06190	lipoxigenase (SC 1
711	6	4.3	743	2	C86168	hypothetical prote	784	6	4.3	938	2	H83050	probable ferredoxi
712	6	4.3	743	2	A29232	101K malaria antiq	785	6	4.3	942	2	T39624	6-phosphofructokin
713	6	4.3	744	2	AF0410	GTP diphosphokinas	786	6	4.3	947	2	T08605	hypothetical prote
714	6	4.3	744	2	AF2582	malate synthase G	787	6	4.3	955	2	T48515	hypothetical prote
715	6	4.3	744	2	F97364	malate synthase G	788	6	4.3	961	2	A55380	faciogenital dyspl
716	6	4.3	747	2	D95862	probable sensor hi	789	6	4.3	963	2	T48707	related to regulat
717	6	4.3	748	2	AD0866	phosphoenolpyruvat	790	6	4.3	980	2	A38523	genome polyprotein
718	6	4.3	749	2	S75331	penicillin-binding	791	6	4.3	981	2	T16060	hypothetical prote
719	6	4.3	750	2	T42614	probable envelope	792	6	4.3	990	2	T11612	hypothetical prote
720	6	4.3	750	2	A84315	malate dehydrogena	793	6	4.3	994	2	T21356	hypothetical prote
721	6	4.3	751	2	F83080	hypothetical prote	794	6	4.3	996	2	JEO237	apolipoprotein E r
722	6	4.3	755	2	H86561	CY456 hypothetical	795	6	4.3	997	2	T15243	hypothetical prote
723	6	4.3	755	2	B72061	fibroblast activat	796	6	4.3	1001	2	T29105	myosin-B - Toxopla
724	6	4.3	759	2	I38593	chemotaxis protein	797	6	4.3	1002	2	T30546	major surface glyc
725	6	4.3	762	2	H87302	hypothetical prote	798	6	4.3	1007	2	T24543	hypothetical prote
726	6	4.3	763	2	T21006	periplasmic beta-g	799	6	4.3	1011	2	T20785	hypothetical prote
727	6	4.3	764	2	F83431	probable transport	800	6	4.3	1013	2	T33470	hypothetical prote
728	6	4.3	769	2	A71403	outer membrane pro	801	6	4.3	1014	2	T30545	proline dehydrogen
729	6	4.3	769	2	F87486	transducer protein	802	6	4.3	1016	2	T31343	DNA-directed DNA p
730	6	4.3	773	2	T44989	neuroendocrine-spe	803	6	4.3	1017	2	T30195	hypothetical prote
731	6	4.3	776	2	A45683	hypothetical prote	804	6	4.3	1018	2	T40253	hypothetical prote
732	6	4.3	778	2	H84578	conserved hypotet	805	6	4.3	1021	2	T23252	hypothetical prote
733	6	4.3	783	2	B83232	probable serine-th	806	6	4.3	1027	2	F87370	alpha-L-rhamnosida
734	6	4.3	783	2	T35389	DNA repair protein	807	6	4.3	1029	2	T05050	protein kinase hom
735	6	4.3	788	1	Q8BEE3	HHuF1 protein - hu	808	6	4.3	1048	2	T23764	hypothetical prote
736	6	4.3	788	1	I51530	integrin beta-3 su	809	6	4.3	1051	2	T05426	probable PPE prote
737	6	4.3	789	1	A45617	6-phosphofructokin	810	6	4.3	1053	2	B70987	kinesin-related pr
738	6	4.3	790	2	T34293	hypothetical prote	811	6	4.3	1060	1	A40264	proline dehydrogen
739	6	4.3	791	2	C95335	hypothetical prote	812	6	4.3	1062	2	H83547	carbamoyl-phosphat
740	6	4.3	792	1	EAHU	elastin precursor,	813	6	4.3	1076	2	T38122	hypothetical prote
741	6	4.3	792	1	EAHU	elastin precursor,	814	6	4.3	1081	2	T09837	sucrose-phosphate
742	6	4.3	793	2	AB1750	exoribonuclease RN	815	6	4.3	1091	1	IJCHNL	neural cell adhesi
743	6	4.3	793	2	AB1380	exoribonuclease RN	816	6	4.3	1091	1	IJCHNL	hypothetical prote
744	6	4.3	795	2	T49835	hypothetical prote	817	6	4.3	1095	2	T20528	myosin-C - Toxopla
745	6	4.3	795	2	T20609	hypothetical prote	818	6	4.3	1098	2	T29106	hypothetical prote
746	6	4.3	796	2	T21460	hypothetical prote	819	6	4.3	1119	2	A86340	protein P210.24 (
747	6	4.3	799	2	S65192	hypothetical prote	820	6	4.3	1120	2	B83498	conserved hypotet
748	6	4.3	802	2	T21315	hypothetical prote	821	6	4.3	1134	1	A29944	chaoptin precursor
749	6	4.3	809	2	F87458	conserved hypotet	822	6	4.3	1145	1	A29944	HIV-1 retropepsin
750	6	4.3	811	2	T19974	hypothetical prote	823	6	4.3	1146	1	GNLJEW	HIV-1 retropepsin
751	6	4.3	813	2	AF0526	ATP-dependent heli	824	6	4.3	1146	1	GNLJ22	HIV-1 retropepsin
752	6	4.3	815	2	JG0197	myosin-light-chain	825	6	4.3	1155	2	G87477	transcription-repa
753	6	4.3	829	2	A34692	ecdysone-induced p	826	6	4.3	1161	2	S57180	probable membrane
754	6	4.3	835	2	A40971	DNA-binding protei	827	6	4.3	1172	2	T00065	hypothetical prote
755	6	4.3	836	2	A13237	conserved hypotet	828	6	4.3	1176	2	A33856	surface-layer 125K
756	6	4.3	837	2	D71027	hypothetical prote	829	6	4.3	1176	2	A49848	nitrite reductase
757	6	4.3	845	2	T34064	hypothetical prote	830	6	4.3	1186	2	S35993	DNA repair protein
758	6	4.3	846	1	QBEC3	HQR1 protein - hu	831	6	4.3	1196	2	S35994	DNA repair protein
759	6	4.3	850	2	T14472	S-receptor kinase	832	6	4.3	1202	2	T17197	adenylate cyclase

833	6	4.3	1206	2	F72233	conserved hypothet	906	6	4.3	3766	2	T29165	hypothetical prote
834	6	4.3	1207	2	B88789	protein ZK1251.9 (907	6	4.3	3972	2	S75251	hypothetical prote
835	6	4.3	1208	2	T23754	hypothetical prote	908	6	4.3	4151	2	T13734	apolipoprotein B-1
836	6	4.3	1211	2	T23210	hypothetical prote	909	6	4.3	4563	1	LPHUB	hypothetical coile
837	6	4.3	1217	2	T00270	co-repressor prote	910	6	4.3	4717	2	T41581	probable membrane
838	6	4.3	1219	2	I61713	hypothetical prote	911	6	4.3	4910	2	S64942	ALR protein - huma
839	6	4.3	1220	1	DJBSC3	DNA-directed DNA p	912	6	4.3	4957	2	T03455	ALR protein - huma
840	6	4.3	1223	2	T42573	protein B0161.3 [i	913	6	4.3	5262	2	T03454	polyketide synthas
841	6	4.3	1222	2	C86504	hypothetical prote	914	6	4.3	5563	2	T30226	T-cell receptor be
842	6	4.3	1224	2	S40977	DNA-directed RNA p	915	5	3.5	10	2	PH0895	bradykinin-potenti
843	6	4.3	1224	2	S73171	DNA-directed RNA p	916	5	3.5	11	2	C37196	bradykinin-potenti
844	6	4.3	1227	2	T48028	hypothetical prote	917	5	3.5	15	2	D37196	lipid transfer pro
845	6	4.3	1228	2	I40468	surface layer prot	918	5	3.5	15	2	A53085	T-cell receptor al
846	6	4.3	1229	2	T25697	hypothetical prote	919	5	3.5	16	2	F11299	hypothetical prote
847	6	4.3	1230	2	A56068	co-repressor prote	920	5	3.5	20	2	T01691	uroporphyrinogen d
848	6	4.3	1234	2	T31523	hypothetical prote	921	5	3.5	27	2	S35595	alpha-1 type-1 col
849	6	4.3	1235	2	T13710	protein-tyrosine k	922	5	3.5	28	2	I50169	hypothetical prote
850	6	4.3	1239	2	I49705	glutamate receptor	923	5	3.5	30	2	C82341	hypothetical prote
851	6	4.3	1251	2	T21389	hypothetical prote	924	5	3.5	32	1	LFEC1	ilvGMDA operon le
852	6	4.3	1252	2	T00263	hypothetical prote	925	5	3.5	32	1	LFEBIT	ilvGMDA leader pep
853	6	4.3	1255	2	T06267	nematodes resistan	926	5	3.5	32	2	E27480	cytochrome-c3 hydr
854	6	4.3	1265	2	T21782	hypothetical prote	927	5	3.5	32	2	E91216	ilvGMDA operon lea
855	6	4.3	1270	2	T13813	hypothetical prote	928	5	3.5	32	2	F86062	ilvGMDA operon le
856	6	4.3	1290	2	T00018	period protein hom	929	5	3.5	32	2	AG0924	ilvGMDA operon at
857	6	4.3	1296	1	HMS01F	aggregation protei	930	5	3.5	34	2	D81044	hypothetical prote
858	6	4.3	1305	2	A40879	phospholipase C (B	931	5	3.5	36	2	C82475	hypothetical prote
859	6	4.3	1305	2	H41562	150K mating aggreg	932	5	3.5	39	2	S65949	hypothetical prote
860	6	4.3	1306	2	S22624	aggregation protei	933	5	3.5	39	2	B55980	hypothetical prote
861	6	4.3	1312	1	B40879	phospholipase C (E	934	5	3.5	41	2	C50288	hypothetical prote
862	6	4.3	1316	2	D87145	[beta] subunit of	935	5	3.5	42	2	T25528	hypothetical prote
863	6	4.3	1316	2	S31146	DNA-directed RNA p	936	5	3.5	43	1	ZDBP79	RhPI-alpha polypep
864	6	4.3	1335	2	T18289	racGAP protein - s	937	5	3.5	45	2	E70236	Gene 55.4 protein
865	6	4.3	1348	2	S27812	probable epidermal	938	5	3.5	45	2	T02336	hypothetical prote
866	6	4.3	1348	2	A43917	probable epidermal	939	5	3.5	45	2	T52271	R4R3-MYB transcrip
867	6	4.3	1356	2	F84486	probable retroelem	940	5	3.5	45	2	T22272	R2R3-MYB transcrip
868	6	4.3	1364	2	T00250	MEG2 protein - hu	941	5	3.5	45	2	T52277	R2R3-MYB transcrip
869	6	4.3	1392	2	T51547	probable transcrip	942	5	3.5	48	2	S27128	histone H1 - sea u
870	6	4.3	1403	2	S64142	hypothetical prote	943	5	3.5	50	2	T06923	high light-inducib
871	6	4.3	1469	2	B36865	slit protein 2 pre	944	5	3.5	51	2	AG1060	aspartic proteinas
872	6	4.3	1480	2	A36665	slit protein 1 pre	945	5	3.5	52	2	T00141	hypothetical prote
873	6	4.3	1489	2	A82524	glutamate synthase	946	5	3.5	52	2	F97078	hypothetical prote
874	6	4.3	1493	2	A38218	GAP-associated pro	947	5	3.5	52	2	AC1894	hypothetical prote
875	6	4.3	1526	2	T41522	myosin ii - fissio	948	5	3.5	54	1	BGSB	spermatid transiti
876	6	4.3	1551	2	T18941	hypothetical prote	949	5	3.5	54	2	A82579	spermatid transiti
877	6	4.3	1589	2	RGBVC5	cell division cont	950	5	3.5	55	1	BQBO	CAB/ELIP/HLIP-rela
878	6	4.3	1589	2	T13606	hypothetical prote	951	5	3.5	56	2	AC2100	hypothetical prote
879	6	4.3	1599	2	C44766	defective chorion-	952	5	3.5	56	2	A95955	hypothetical prote
880	6	4.3	1639	2	T14181	peptide synthetase	953	5	3.5	57	2	H84366	hypothetical prote
881	6	4.3	1655	2	T13298	gene mastermind pr	954	5	3.5	57	2	AG3000	hypothetical prote
882	6	4.3	1706	2	B75633	probable RNA helic	955	5	3.5	57	2	AG0134	hypothetical prote
883	6	4.3	1711	1	A55148	protein-tyrosine-p	956	5	3.5	58	1	TVHUB	transforming prote
884	6	4.3	1731	2	AB3045	ice nucleation pro	957	5	3.5	58	2	C84363	ferredoxin import
885	6	4.3	1731	2	B98241	hypothetical prote	958	5	3.5	58	2	AE1868	hypothetical prote
886	6	4.3	1839	1	OFBFX	adenylate cyclase	959	5	3.5	59	2	G71717	hypothetical prote
887	6	4.3	1921	2	T13827	kinesin-73 - fruit	960	5	3.5	60	2	C29606	hypothetical prote
888	6	4.3	2108	2	H70819	probable polyketid	961	5	3.5	61	2	JT0460	hypothetical prote
889	6	4.3	2123	2	S55089	probable acetyl-Co	962	5	3.5	62	2	A26878	tyrocidine synthet
890	6	4.3	2204	1	RRN2V	genome polyprotein	963	5	3.5	62	2	AP3474	ubiquinol-cytochro
891	6	4.3	2244	2	T08212	DNA-directed RNA p	964	5	3.5	63	2	F84284	hypothetical prote
892	6	4.3	2348	2	AD1841	hypothetical prote	965	5	3.5	63	2	T43546	DNA-directed RNA p
893	6	4.3	2396	2	T13714	kakapo gene protei	966	5	3.5	63	2	T52536	DNA-directed RNA p
894	6	4.3	2500	2	G88493	protein F57B9.2 [i	967	5	3.5	65	2	T42904	hypothetical prote
895	6	4.3	2524	2	A35844	Xotch protein - Af	968	5	3.5	65	2	S77379	hypothetical prote
896	6	4.3	2555	2	A40043	notch protein homo	969	5	3.5	65	2	H83679	hypothetical prote
897	6	4.3	2569	2	T14164	peptide synthetase	970	5	3.5	66	2	H87276	hypothetical prote
898	6	4.3	2639	2	T31328	fibroin - Chinese	971	5	3.5	66	2	AH0076	hypothetical prote
899	6	4.3	2670	2	A46719	inositol 1,4,5-tri	972	5	3.5	66	2	T08651	hypothetical prote
900	6	4.3	2671	2	A49873	inositol 1,4,5-tri	973	5	3.5	67	2	T86888	hypothetical prote
901	6	4.3	2833	2	A43360	inositol 1,4,5-tri	974	5	3.5	67	2	T17830	alkaline phosphata
902	6	4.3	2918	2	A54105	fibryllin-2 precu	975	5	3.5	67	2	H69991	hypothetical prote
903	6	4.3	3172	2	S22012	erythronolide synt	976	5	3.5	67	2		
904	6	4.3	3178	2	S13595	6-deoxyerythronol	977	5	3.5	67	2		
905	6	4.3	3355	2	G81702	adherence factor T	978	5	3.5	67	2		

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979      5      3.5      67      2      T36348
980      5      3.5      67      2      AF1915
981      5      3.5      67      2      A12190
982      5      3.5      70      1      C11482
983      5      3.5      70      2      S76161
984      5      3.5      70      2      T30707
985      5      3.5      71      2      B81812
986      5      3.5      71      2      T42025
987      5      3.5      72      2      C90896
988      5      3.5      72      2      C90896
989      5      3.5      72      2      D85721
990      5      3.5      72      2      C47072
991      5      3.5      72      2      AG2793
992      5      3.5      73      2      H72866
993      5      3.5      73      2      AB2394
994      5      3.5      74      2      T43671
995      5      3.5      74      2      H69608
996      5      3.5      74      2      H87339
997      5      3.5      74      2      AC3186
998      5      3.5      75      2      E69508
999      5      3.5      75      2      A64698
1000     5      3.5      75      2      D75300

ALIGNMENTS

RESULT 1
T14194
extensin homolog T28D5.90 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-Jan-2000
C:Accession: T14194
R:Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancro
submitted to the Protein Sequence Database, August 1999
A:Reference number: Z17931
A:Accession: T14194
A:Molecule type: DNA
A:Residues: 1-513 <BEV>
A:Cross-references: EMBL:AL109819
A:Experimental source: cultivar Columbia; BAC clone T28D5
C:Genetics:
A:Gene: ATSP:T28D5.90
A:Map position: 4
C:Superfamily: hydroxyproline-rich glycoprotein

Query Match      5.7%; Score 8; DB 2; Length 513;
Best Local Similarity 100.0%; Pred.No. 4.9;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      59 SAIAATVT 66
DB      23 SAIAATVT 30
|||||

RESULT 2
G84642
hypothetical protein At2g24980 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 03-Jun-2002
C:Accession: G84642
R:Linn, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: G84642
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-559 <STO>
A:Cross-references: GB:AE002093; NID:g4559354; PIDN:AAD23015.1; GSPDB:GN00139
C:Genetics:

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A:Gene: At2g24980
A:Map position: 2
C:Superfamily: hydroxyproline-rich glycoprotein

Query Match      5.7%; Score 8; DB 2; Length 559;
Best Local Similarity 100.0%; Pred.No. 5.3;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      59 SAIAATVT 66
DB      14 SAIAATVT 21
|||||

RESULT 3
T14195
extensin homolog T28D5.100 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 29-Oct-1999
C:Accession: T14195
R:Bevan, M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Banci
submitted to the Protein Sequence Database, August 1999
A:Reference number: Z17931
A:Accession: T14195
A:Molecule type: DNA
A:Residues: 1-707 <BEV>
A:Cross-references: EMBL:AL109819
A:Experimental source: cultivar Columbia; BAC clone T28D5
C:Genetics:
A:Gene: ATSP:T28D5.100
A:Map position: 4

Query Match      5.7%; Score 8; DB 2; Length 707;
Best Local Similarity 100.0%; Pred.No. 6.6;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      59 SAIAATVT 66
DB      41 SAIAATVT 48
|||||

RESULT 4
T2893
hypothetical protein B2168 C2_205 - Mycobacterium leprae
C:Species: Mycobacterium leprae
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C:Accession: S72893
R:Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A:Description: Mycobacterium leprae cosmid B2168.
A:Reference number: S72586
A:Accession: S72893
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-105 <SMI>
A:Cross-references: EMBL:U00018; NID:g467037; PIDN:AAAI7229.1; PID:g467045
C:Genetics:
A:Start codon: GTG

Query Match      5.0%; Score 7; DB 2; Length 105;
Best Local Similarity 100.0%; Pred.No. 13;
Matches      7; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      43 ALAGMCG 49
DB      42 ALAGMCG 48
|||||

RESULT 5
S73004
hypothetical protein B229 F2_64 - Mycobacterium leprae
C:Species: Mycobacterium leprae
C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
C:Accession: S73004

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R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B229.
A;Reference number: S72588
A;Accession: S73004
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-148 <SMI>
A;Cross-references: EMBL:U00020; NID:g467102; PIDN:AAA17318.1; PID:g4671136

Query Match 5.0%; Score 7; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 17; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 3 STSTTTN 9
|||||
DB 85 STSTTTN 91

RESULT 6
A40669

Mitochondrial receptor complex chain MOM22 - Neurospora crassa
N;Alternate names: mitochondrial outer membrane preprotein receptor chain MOM22
C;Species: Neurospora crassa
C;Date: 03-May-1994 #sequence_revision 02-Jun-1994 #text_change 22-Jun-1999
C;Accession: A40669; S33472
R;Kiebler, M.; Keil, P.; Schneider, H.; van der Klei, I.J.; Pfanner, N.; Neupert, W.
Cell 74, 483-492, 1993
A;Title: The mitochondrial receptor complex: a central role of MOM22 in mediating prepro
A;Reference number: A40669; MUID:93351229; PMID:8348615
A;Accession: A40669
A;Molecule type: mRNA
A;Residues: 1-154 <KIE>
A;Cross-references: GB:X71021; NID:g311426; PIDN:CAA50339.1; PID:g311427
C;Comment: This protein resides in the mitochondrial outer membrane (MOM) where it serve
C;Genetics:
A;Gene: MOM22
C;Superfamily: mitochondrial receptor complex chain MOM22
C;Keywords: mitochondrion; transmembrane protein
F;85-105/Domain: transmembrane #status predicted <TMM>

Query Match 5.0%; Score 7; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 18; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 5 STTTNFV 11
|||||
DB 69 STTTNFV 75

RESULT 7
B57055

melanocortin-4 receptor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 07-May-1999
C;Accession: B57055
R;Moutjoy, K.G.; Mortrud, M.T.; Low, M.J.; Simerly, R.B.; Cone, R.D.
Mol. Endocrinol. 8, 1298-1308, 1994
A;Title: Localization of the melanocortin-4 receptor (MC4-R) in neuroendocrine and auton
A;Reference number: A57055; MUID:95157557; PMID:7854347
A;Accession: B57055
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-215 <MOU>
C;Superfamily: melanocortin receptor

Query Match 5.0%; Score 7; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 24; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 52 VLPGTCA 58
|||||
DB 151 VLPGTGA 157

RESULT 8
A33619

Transcription regulator, gntR family BME110878 [imported] - Brucella melitensis (strain: A33619)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: A33619
R;DelVecchio, V.G.; Kapural, V.; Redkar, R.J.; Patra, G.; Mujter, C.; Los, T.; Ivanova, M.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Lete
Proc Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliter
A;Reference number: A33619; PMID:11756688
A;Accession: A33619
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-237 <KUR>
A;Cross-references: GB:AE008918; PIDN:AAU54120.1; PID:g17985081; GSPDB:GN00191
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BME110878
A;Map position: 11

Query Match 5.0%; Score 7; DB 2; Length 237;
Best Local Similarity 100.0%; Pred. No. 27; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 25 MREALLR 31
|||||
DB 69 MREALLR 75

RESULT 9
H71291

probable flagellar motor rotation protein (motB) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jun-2000
C;Accession: H71291
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gw
ron, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McI
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: H71291
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-238 <COL>
A;Cross-references: GB:AE001244; GB:AE000520; NID:g3323005; PIDN:AAC65689.1; PID:g33230
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: Tp0724
C;Superfamily: probably motility protein ytxE

Query Match 5.0%; Score 7; DB 2; Length 238;
Best Local Similarity 100.0%; Pred. No. 27; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

QY 26 REALLRV 32
|||||
DB 138 REALLRV 144

RESULT 10
D70748

Probable formamidopyrimidine-dna glycosylase - Mycobacterium tuberculosis (strain H37Rv)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: D70748
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, J.; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998

A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Reference number: A70500; MUID:98295987; PMID:9634230
 A;Accession: D70748
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-289 <COL>
 A;Cross-references: GB:274697; GB:AL123456; NID:G3261602; PIDN:CAA98987.1; PID:G3261604
 A;Experimental source: strain H37Rv
 C;Genetics:
 A;Gene: fpg
 C;Superfamily: formamidopyrimidine-DNA glycosylase

Query Match 5.0%; Score 7; DB 2; Length 289;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 DVMREAL 29
 Db 219 DVMREAL 225

RESULT 11
 AH0552
 protein-export membrane protein SecF [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AH0552
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, P.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; White, N.; Wilson, D.; Young, L.; Ziegler, W.
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AH0552
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-323 <PAR>
 A;Cross-references: GB:AL513382; PIDN:CAD08864.1; PID:G16501677; GSPDB:GN00176
 C;Genetics:
 A;Gene: STY0446
 C;Superfamily: Escherichia coli preproteins translocase chain secF

Query Match 5.0%; Score 7; DB 2; Length 323;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 DVMREAL 29
 Db 69 DVMREAL 75

RESULT 12
 G83517
 Probable glycosyl transferase PA1014 [imported] - Pseudomonas aeruginosa (strain PA01)
 C;Species: Pseudomonas aeruginosa
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: G83517
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Broun, A.; Buchanan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
 A;Reference number: AB2950; MUID:20437337; PMID:10984043
 A;Accession: G83517
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-330 <STO>
 A;Cross-references: GB:AE004534; GB:AE004091; NID:G9946924; PIDN:AA04403.1; GSPDB:GN001
 A;Experimental source: strain PA01
 C;Genetics:

A;Gene: PA1014

Query Match 5.0%; Score 7; DB 2; Length 330;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ERLAMLR 42
 Db 79 ERLAMLR 85

RESULT 13
 AS7055
 melanocortin receptor 4 - human
 C;Species: Homo sapiens (man)
 C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 24-Sep-1999
 C;Accession: AS7055; A47111
 R;Mountjoy, K.G.; Mortrud, M.T.; Low, M.J.; Simerly, R.B.; Cone, R.D.
 Mol. Endocrinol. 8, 1298-1308, 1994
 A;Title: Localization of the melanocortin-4 receptor (MC4-R) in neuroendocrine and autonomic nervous system
 A;Reference number: AS7055; MUID:95157557; PMID:7854347
 A;Accession: AS7055
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-332 <MOU>
 A;Cross-references: GB:S77415; NID:9998456; PIDN:AA83341.1; PID:9998457
 R;Gantz, I.; Miwa, H.; Konda, Y.; Shimoto, Y.; Tashiro, T.; Watson, S.J.; Delvalle, J.
 J. Biol. Chem. 268, 15174-15179, 1993
 A;Title: Molecular cloning, expression, and gene localization of a fourth melanocortin receptor
 A;Reference number: A47111; MUID:93315499; PMID:8392067
 A;Accession: A47111
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-168, '1' 170-332 <GAN>
 A;Cross-references: GB:L08603; NID:9291977; PIDN:AAA35791.1; PID:9291978
 C;Genetics:
 A;Gene: GDB:MC4R
 A;Cross-references: GDB:203939; OMIM:155541
 A;Map position: 20q13.2-20q13.3
 C;Superfamily: melanocortin receptor
 C;Keywords: hormone receptor

Query Match 5.0%; Score 7; DB 2; Length 332;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 VLPGTGA 58
 Db 228 VLPGTGA 234

RESULT 14
 G90291
 endoglucanase precursor [imported] - Sulfolobus solfataricus
 C;Species: Sulfolobus solfataricus
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
 C;Accession: G90291
 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chai, J.; Jorgensen, R.A.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.
 submitted to GenBank, April 2001
 A;Description: Sulfolobus solfataricus complete genome.
 A;Reference number: A99139
 A;Accession: G90291
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-332 <KUR>
 A;Cross-references: GB:AE006641; NID:G13814564; PIDN:AAK41590.1; GSPDB:GN00155
 C;Genetics:
 A;Gene: SSO1354

Query Match 5.0%; Score 7; DB 2; Length 332;
 Best Local Similarity 100.0%; Pred. No. 36;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 STSTTN 9
|||||

Db 45 STSTTN 51

RESULT 15

B83303
phenylalanyl-tRNA synthetase, alpha-subunit PA2740 [imported] - Pseudomonas aeruginosa
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: B83303
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: B83303
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-338 <STO>
A:Cross-references: GB:AE004702; GB:AE004091; NID:G9948813; PIDN:AA06128.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: pheS; PA2740
C:Superfamily: phenylalanine-tRNA ligase alpha chain

Query Match 5.0%; Score 7; DB 2; Length 338;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ERLAMLR 42
|||||

Db 311 ERLAMLR 317

RESULT 16

T34158
Hypothetical protein C42D4.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T34158
R:Du, Z.; Le, T.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid C42D4.
A:Reference number: Z21483
A:Accession: T34158
A>Status: Preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-339 <DUZ>
A:Cross-references: EMBL:U41991; PIDN:AA083342.1; CESP:C42D4.6
C:Genetics:
A:Gene: CESP:C42D4.6
A:Introns: 135/1; 158/3

Query Match 5.0%; Score 7; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 RKIREMN 98
|||||

Db 79 RKIREMN 85

RESULT 17

S22366
phenylalanine-tRNA ligase (EC 6.1.1.20) alpha chain [validated] - Thermus aquaticus
N:Alternate names: phenylalanyl-tRNA synthetase alpha chain
C:Species: Thermus aquaticus
C>Date: 22-Nov-1993 #sequence_revision 23-Feb-1996 #text_change 03-Jun-2002
C:Accession: S22366; S25717; S61093; T52502; S21468

R;Keller, B.; Kast, P.; Hennecke, H.
FEBS Lett. 301, 83-89, 1992
A:Title: Cloning and sequence analysis of the phenylalanyl-tRNA synthetase genes (pheST
A:Reference number: S22366; MUID:93083630; PMID:1451792
A:Accession: S22366
A:Molecule type: DNA
A:Residues: 1-350 <KEL>
A:Cross-references: EMBL:Z12118; NID:G48253; PIDN:CAA78104.1; PID:G48254
A:Note: the source is designated as Thermus thermophilus
R;Kreutzer, R.; Kruff, V.; Bobkova, E.V.; Lavrik, O.I.; Sprinzl, M.
Nucleic Acids Res. 20, 4173-4178, 1992
A:Title: Structure of the phenylalanyl-tRNA synthetase genes from Thermus thermophilus
A:Reference number: S25717; MUID:92375722; PMID:1508711
A:Accession: S25717
A:Molecule type: DNA
A:Residues: 1-350 <KRE>
A:Cross-references: EMBL:X65609; NID:G48250; PIDN:CAA46559.1; PID:G48251
A:Experimental source: strain HB8 (ATCC 27634)
A:Note: the source is designated as Thermus thermophilus
A:Accession: S61093
A:Molecule type: protein
A:Residues: 1-29 <KRW>
R;Lechler, A.; Kreutzer, R.
J. Mol. Biol. 278, 897-901, 1998
A:Title: The phenylalanyl-tRNA synthetase specifically binds DNA.
A:Reference number: Z26096
A:Accession: T52502
A>Status: Preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-350 <LEC>
A:Cross-references: EMBL:Y15464; PIDN:CAA75644.1
A:Experimental source: strain HB8
C:Genetics:
A:Gene: pheS
C:Function:
A:Description: EC 6.1.1.20 [validated, MUID:98263257]; binds specifically certain DNA s
C:Superfamily: phenylalanine-tRNA ligase alpha chain
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 5.0%; Score 7; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 ERLAMLR 42
|||||

Db 320 ERLAMLR 326

RESULT 18

S45887
ribosomal protein L4.e.A, cytosolic - Yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YBR0315; protein YBR031w; ribosomal protein rp2; ribosomal p
C:Species: Saccharomyces cerevisiae
C>Date: 26-Aug-1994 #sequence_revision 09-Sep-1994 #text_change 13-Aug-1999
C:Accession: S45887; S46561; A28656; S45500
R;Grivell, L.A.; de Haan, M.; Maat, M.J.; Smits, P.H.M.
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45875
A:Accession: S45887
A:Molecule type: DNA
A:Residues: 1-362 <GRI>
A:Cross-references: EMBL:Z35900; NID:G536243; PIDN:CAA84973.1; PID:G536244; MIPS:YBR031
A:Experimental source: strain S288C
R;Smits, P.H.M.; de Haan, M.; Maat, C.; Grivell, L.A.
Yeast 10(Suppl.A), S75-S80, 1994
A:Title: The complete sequence of a 33 kb fragment on the right arm of chromosome II fr
ly identified genes and a homologue of the SCO1 gene.
A:Reference number: S46551; MUID:94378725; PMID:8091864
A:Accession: S46561
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-362 <SMI>
A:Cross-references: EMBL:X76078; NID:G498748; PIDN:CAA53687.1; PID:G498759

R;Eide, L.G.; Sander, C.; Prydz, H.
Yeast 12, 1085-1090, 1996
A>Title: Sequencing and analysis of a 35.4 kb region on the left arm of chromosome IV
A:Reference number: S72107; MUID:97051598; PMID:8896275
A:Accession: S72110
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-362 <EW>
A:Cross-references: EMBL:X95966; NID:g1216215; PIDN:CAA65204.1; PID:g1216219
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
C:Genetics:
A:Gene: SGD:RPL2B
A:Cross-references: MIPS:YDR012w; SGD:S0002419
A:Map position: 4R
C:Superfamily: rat ribosomal protein L4
C:Keywords: cytosol; protein biosynthesis; ribosome

Query Match 5.0% Score 7; DB 2; Length 362;
Best Local Similarity 100.0%; Pred.No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 58 ASAAAT 64
 |||||
Db 123 ASAAAT 129

RESULT 20
BVBYK2
MAK32 protein - yeast (Saccharomycetes cerevisiae)
N:Alternate names: protein YCR019w
C:Species: Saccharomycetes cerevisiae
C>Date: 30-Jun-1991 #sequence_revision 30-Sep-1993 #text_change 16-Jun-2000
C:Accession: S19429; S07695
R:Feldmann, H.; Mannhaupt, G.; Vetter, I.
submitted to the Protein Sequence Database, March 1992
A:Reference number: S19429
A:Accession: S19429
A:Molecule type: DNA
A:Residues: 1-363 <FEL>
A:Cross-references: EMBL:X59720; NID:g1907116; PIDN:CAA42310.1; PID:g1907162; GSPDB:GNCN
R:Toh-e, A.; Sahara, Y.
Yeast 1, 159-171, 1985
A>Title: The Pfl8 locus of Saccharomycetes cerevisiae: a complex locus containing multiple
A:Reference number: S07692; MUID:89131254; PMID:3916862
A:Accession: S07695
A:Molecule type: DNA
A:Residues: 1-14, 'I', 15-81, 83-282, 'S', 284-363 <TOH>
C:Genetics:
A:Gene: SGD:MAX32; MIPS:YCR019w
A:Cross-references: SGD:S0000612; MIPS:YCR019w
A:Map position: 3R
C:Superfamily: MAK32 protein

Query Match 5.0% Score 7; DB 1; Length 363;
Best Local Similarity 100.0%; Pred.No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 LLRVKSS 35
 |||||
Db 158 LLRVKSS 164

RESULT 21
AD1188
membrane proteins homolog lmc0908 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AD1188
R:Glaser, P.; Frauguel, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Psihi, I.
J.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J., Kubo
A:Keywords: kreft, J., Kubo